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OM nucleic - nucleic search, using sw model

December 31, 2006, 12:26:03 Run on:

; Search time 132.37 Seconds (without alignments) 6266.684 Million cell updates/sec

US-09-232-880-67 385

1 actacacactccacttgc......tttctgtgctagtggaccgt 385 Title: Perfect score:

Scoring table: Sequence:

3050214 seqs, 1077301958 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

6100428 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications NA New: Database :

1. FEMC Celerra SIDS3/prodata/2/pubpna/US09_NEW_PUB.seq:*
2. FEMC Celerra SIDS3/prodata/2/pubpna/US06_NEW_PUB.seq:*
3. FEMC Celerra SIDS3/prodata/2/pubpna/US06_NEW_PUB.seq:*
3. FEMC Celerra SIDS3/prodata/2/pubpna/US08_NEW_PUB.seq:*
3. FEMC Celerra SIDS3/prodata/2/pubpna/PCT_NEW_PUB.seq:*
3. FEMC Celerra SIDS3/prodata/2/pubpna/US10_NEW_PUB.seq:*
3. FEMC Celerra SIDS3/prodata/2/pubpna/US11_NEW_PUB.seq:*
3. FEMC Celerra SIDS3/prodata/2/pubpna/US11_NEW_PUB.seq:*
3. FEMC Celerra SIDS3/prodata/2/pubpna/US11_NEW_PUB.seq:*
4. FEMC Celerra SIDS3/prodata/2/pubpna/US11_NEW_PUB.seq:* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		ф			SUMMARIES	
Result No.	Score	Query Match	Query Match Length	08	ID	Description
<u> </u>	385	100.0	385	7	US-11-344-932-67	Sequence 67, Appl
~	385	100.0	385	10	US-11-349-541-67	~
٣	307.2	79.8	3228	7	US-11-344-932-701	Sequence 701, App
4	231.8	60.2	1016	80	US-11-266-748A-350613	Sequence 350613,
S	231.8	60.2	1016	80	US-11-266-748A-383047	Sequence 383047,
9	231.8	60.2	1016	80	US-11-266-748A-433992	Sequence 433992,
7	107.4	27.9	2841	7	US-11-344-932-700	Sequence 700, App
8	95	24.7	1016	æ	US-11-266-748A-350613	Sequence 350613,
σ	95	24.7	1016	œ	US-11-266-748A-383047	Sequence 383047,
01	95	24.7	1016	60	US-11-266-748A-433992	Sequence 433992,
11	89.2	23.2	5449	œ	US-11-266-748A-32477	Sequence 32477, A
7	84	21.8	385	7	US-11-344-932-67	Sequence 67, Appl
13	84	21.8	385	10	US-11-349-541-67	Sequence 67, Appl
14	77.2	20.1	25694	ø	US-10-669-920-46	Sequence 46, Appl
15	75.2	19.5	154394	8	US-11-266-748A-58517	Sequence 58517, A
16	73.8	19.2	80988	9	US-10-669-920-261	Sequence 261, App
11	73.8	19.2	421987	8	US-11-266-748A-28210	Sequence 28210, A
18	70.4	18.3	3228	7	US-11-344-932-701	Sequence 701, App
13	9.69	18.1	593	8	US-11-266-748A-254460	
20	9.69	18.1	593	8	US-11-266-748A-314977	Seguence 314977,
21	9.79	17.6	198285	œ	US-11-266-748A-59857	Sequence 59857, A
52	9.79	17.6	4647455	9	US-10-641-321-205	Sequence 205, App

	Sequence 29045, A	Sequence 200795,	Sequence 11257, A	Sequence 57638, A	Sequence 700, App	Sequence 29041, A	Sequence 22664, A	Sequence 60144, A	Seguence 196189,	Sequence 1613, Ap	Sequence 24171, A	Sequence 29041, A	Sequence 11257, A	Sequence 57638, A	Sequence 28210, A	Sequence 1140, Ap	Sequence 1151, Ap	Sequence 203066,	Sequence 699, App	Sequence 32477, A	Sequence 22, Appl	Sequence 4, Appli	
US-11-371-354-11185	US-11-266-748A-29045	US-11-266-748A-200795	US-11-371-354-11257	US-11-266-748A-57638	US-11-344-932-700	US-11-266-748A-29041	US-11-266-748A-22664	US-11-266-748A-60144	US-11-266-748A-196189	US-11-073-360-1613	US-11-266-748A-24171	US-11-266-748A-29041	US-11-371-354-11257	US-11-266-748A-57638	US-11-266-748A-28210	US-10-669-920-1140	US-10-669-920-1151	US-11-266-748A-203066	US-11-344-932-699	US-11-266-748A-32477	US-11-330-648-22	US-10-669-920-4	
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6.7	9.9	16.3	16.3	16.3	9.9	5.4	5.3	15.3	13.8	13.8	13.5	13.4	13.0	13.0	12.9	12.8	12.8	12.6	12.5	2.5	12.3	12.3	
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64.2	63.8	62.6	62.6	62.6	9	59.2	59	58.8	53.2	53	52	51.6	50.2	50.2	49.8	49.4	49.4	48.4	48	48	47.4	47.4	
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ALIGNMENTS

RESULT 1

US-11-344-932-67	Sequence 67, Application US/11344932 Publication No. US20060269532A1	GENERAL INFORMATION:	: Xu, Jiangchun	: Dillon, Davin C.	: Mitcham, Jennifer		: Jiang, Yuqiu	: Hender		ranger, cary	APPLICANT: Retter, Marc W. APPLICANT: Stolk John A.	Day Craid		: Cart		: Wang, Aijun	: Skeiky, Yasir A.	: Hepler,	: Hural, John	: McNeill, Patricia	: Houghton, Raymond L.	· 		: Watanabe, Yoshihiro	APPLICANT: Meagher, Madeleine Joy	JANT: Deng, Ta	OF INVENTION: C		FILE REFERENCE: 210121.427C32	CURKENI AFFLICATION NUMBER: US/11/344,932		AFFLICATION NUMBER:	A MOTTAGE TORIES	FILING DATE: 2001-12-10	ADDITIONATION A	FILING DATE: 2001-06-29	APPLICATION N	FILING DATE: 2001-05-09	APPLICATION N	PRIOR FILING DATE: 2001-02-09	
US-11-3	; Seque:	GENER	; APPL	; APPL	, APPL.	, APPL	APPL	, APPL	APPL	APPL.	APPL	APPI	APPL	, APPL	, APPL	, APPL	, APPL	, APPL	, APPL	APPL	, APPL	APPL	APPL	, APPL	APPL	, APPL	TITE	TIL	FILE	; CURR	; CUKK	PATO.	OTRIG.	DIAG .	CTGG .	OTAG .	PRIO	PRIO	PRIO	PRIO	

AND

us-09-232-880-67.rnpbn

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241 CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
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APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
                                                                                                                                                                                                                    Ouery Match 100.0%; Score 385; DB 10; Best Local Similarity 100.0%; Pred. No. 2.9e-119; Matches 385; Conservative 0; Mismatches 0;
PRIOR FILING DATE: 1997-02-25
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 CATAGTTTCTGTGCTAGTGGACCGT 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 701, Application US/11344932; Publication No. US20060269532A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals y de Bassols, C
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Meagher, Madeleine Joy
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Hepler, William T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang, Aijun
                                                                                                                            TYPE: DNA ORGANISM: Homo sapien
                                                                                                                                                                            US-11-349-541-67
                                                                                                     LENGTH: 385
                                                                            SEQ ID NO 67
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APPLICANT:
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APPLICANT:
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SEQUENCE 67, Application US/11349541

SEQUENCE 67, Application No. US20060223129A1

GENERAL INCORMATION:
APPLICANT: U. Jiangchun

TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND
TITLE OF INVENTION: METHODS FOR THEIR USE
FILE REFERENCE: 210121.428C7

CURRENT APPLICATION NUMBER: US/11/349,541

CURRENT FILING DATE: 1998-07-14

PRIOR APPLICATION NUMBER: US 09/116,134

PRIOR FILING DATE: 1998-07-14

PRIOR FILING DATE: 1998-02-25

PRIOR FILING DATE: 1998-02-25

PRIOR FILING DATE: 1998-02-09

PRIOR PLILNG DATE: 1997-08-01

PRIOR PLILNG DATE: US 08/806,596
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                    PRIOR FILING DATE: 2001-01-12
PRIOR PLILAG DATE: 2000-10-09
PRIOR APPLICATION NUMBER: 09/709,729
PRIOR PILING DATE: 2000-11-09
PRIOR PELING DATE: 2000-10-10
PRIOR PELING DATE: 2000-10-10
PRIOR PELING DATE: 2000-10-00
PRIOR FILING DATE: 2000-10-00
PRIOR PILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR FILING DATE: 2000-00-06
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100.0%; Score 385; DB 7; L
Best Local Similarity 100.0%; Pred. No. 2.9e-119;
Matches 385; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                              ), ORGANISM: Homo sapiens
US-11-344-932-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-11-349-541-67
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Gaps

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Length 385; Indels

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GENERAL INFORMATION:

APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Malligan, Karl
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 5815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2005-03-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (954). (972)
OTHER INFORMATION: n is a, c,
US-11-266-7488-350613
  Publication No. US20060134663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo Sapiens
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LOCATION: (880)..(881)
OTHER INFORMATION: n is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 79.8%; Score 307.2; DB 7; Length 3228; Best Local Similarity 92.0%; Pred. No. 1.4e-92; Matches 346; Conservative 0; Mismatches 28; Indels 2;
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
             NAME/KEY: misc_feature
i_CCATION: 66, 2343, 2387, 3065
i_CTHER INFORMATION: n = A,T,C or G
US-11-344-932-701
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                                                                                                                                            Gaps
                                                                                                                                            4;
                                                                                   Length 1016;
                                                                                                                                            32; Indels
                                                                             60.2%; Score 231.8; DB 8;
88.0%; Pred. No. 1.9e-67;
Live 0; Mismatches 32;
g, or
                                                                             Query Match
Best Local Similarity 88.0°
Matches 265; Conservative
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RESULT 5 US-11-266-748A-383047/c

RESULT 4 US-11-266-748A-350613/c ; Sequence 350613, Application US/11266748A

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                                                                    APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 58815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
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Sequence 383047, Application US/11266748A
Publication No. US20060134663A1
GENERAL INFORMATION:
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LOCATION: (964).. (972)
CTHER INFORMATION: n is a, c, g, or t
US-11-266-7488-383047
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OTHER INFORMATION: n is a,
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                                                                                STREAKL INVOCATION Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPRENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105492.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-03-14
Sequence 433992, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature; LOCATION: (137); CTHER INFORMATION: n is a, c, g, US-11-266-748A-433992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (45)...(53)
OTHER INFORMATION: n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G 311
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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169 GGAGTGCTGATATCAGACCAGCCCCATCTCATGTGCAGGACTGCCCAGCAGAGATCAGGT 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 crcadadeagaacrercaaaadreaacccceecacaeacaradererrracaaac 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 TCTTTAGAGGCTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTT 290
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1364 CAGGGCACTCTCAGATGCCCATAGTTTCTGTGCTAGTGGACCGT 1412
                                                                                                                                                                                                                                                                                                                       APPLICANT: HOUSEALION:
APPLICANT: Johnston, Patrick
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 58815-0102 (319189)
CURRENT FILING DATE: 2005-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-01-14
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-07-18
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
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Pred. No. 2.2e-21;
0; Mismatches 80; Indels
                                                                             337 CAGGGCACTCTCAGATGCCCATACCATAGTTTCTGTGCTAGTGGACCGT
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                                                                                                                                                                                                                                                  Sequence 350613, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
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Best Local Similarity 65.1%;
Matches 157; Conservative
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; LOCATION: (964]..(972)
; OTHER INFORMATION: n is a,
US-11-266-748A-350613
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ORGANISM: Homo Sapiens
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LOCATION: (880)..(881)
                                                                                                                                                                                                  RESULT 8
US-11-266-748A-350613
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SEQ ID NO 350613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2841;
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99.1%; Pred. No. 2.6e-25;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 210121.427032
CURRENT APPLICATION NUMBER: US/11/344,932
CURRENT FILING DATE: 2006-02-01
PRIOR APPLICATION NUMBER: 10/144,678
PRIOR APPLICATION NUMBER: 10/102,896
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 09/895,814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McNeill, Patricia D.
Houghton, Raymond L.
Vinals y de Bassols, Carlota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-02-09
RIOR APPLICATION NUMBER: 09/759,143
PRIOR FILING DATE: 2001-01-12
RIOR APPLICATION NUMBER: 09/709,729
RIOR FILING DATE: 2000-11-09
RIOR APPLICATION NUMBER: 09/685,166
PRIOR FILING DATE: 2000-10-10
RIOR PAPLICATION NUMBER: 09/679,426
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/852,911
PRIOR FILING DATE: 2001-05-09
                                                     Application US/11344932
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Meagher, Madeleine Joy
Deng, Ta
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US-11-344-932-700
                                                                                                                          APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
                                                                                                                                                                                                                             Jiang, Yuqiu
Henderson, Robert A.
Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skeiky, Yasir A. W.
Hepler, William T.
                                                                                                                                                                                                                                                                                                                                                                                  Jay, Craig H.
Jedvick, Thomas S.
Jarter, Darrick
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Best Local Similarity 99.19
Matches 108; Conservative
                                                                                                                                                                                                                                                                                                            Panger, Gary R. Retter, Marc W.
                                                                                                                                                                                                                                                                                                                                                            John A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Samuel X
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ORGANISM: Homo sapiens
                                               Sequence 700, Applica
Publication No. US200
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 cicadadenanciercentanancientenance 288
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APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Partick
APPLICANT: Johnston, Partick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: ED 44105479.2
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PELING DATE: 2005-03-14
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65.1%; Pred. No. 2.2e-21;
ive 0; Mismatches 80; Indels
                                                                                                                                                                         Sequence 383047, Application US/11266748A
Publication No. US20060134663A1
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LOCATION: (964)...(972)
CTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-383047
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OTHER INFORMATION: n is a,
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Best Local Similarity 65.13
Matches 157; Conservative
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291 A 291
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LENGTH: 1016
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111 CTGAGAGTTCCCCTTTTAAAAAGGGGACTTGCTTAAAAAAGAAGTCTAGCCACGATTGT 170 788 cicadadesanciercicanandia de cecesacacacacatades en 129 728 Argeccaegerrerriringadeaagrecerriringaagagagaacreregaacrea 231 TCTTTAGAGGCTGGGGAGTCTTGCACATGAGATGGGGGCTGGTCTGATCTCAGCACTCCTT 290 51 GGAATGCTGAGGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGT 171 GTAGAGCAGCIGIGCIGIGCIGGAGAIICACTITIGAGAGAGITCTCCTCTGAGACCTGA Gaps 4; GENERAL INCOGRATION:
JAPPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Methods of Using the Same
CURRENT APPLICATION NUMBER: ED 04105479.2
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-01-14
PRIOR FILING DATE: 2005-01-14
PRIOR FILING DATE: 2005-07-18
PRIOR PILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18
PRIOR FILING DATE: 2005-07-18 Length 1016; 80; Indels Score 95; DB 8; I Pred. No. 2.2e-21; 0; Mismatches 80; Sequence 433992, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION: or 占 ģ ģ NAME/KEY: misc feature LOCATION: (137) OTHER INFORMATION: n is a, c, US-11-266-7488-433992 Query Match
24.7%;
Best Local Similarity 65.1%;
Matches 157; Conservative C ΰ OTHER INFORMATION: n is a, NAME/KEY: misc feature ORGANISM: Homo Sapiens

110

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48 TTAGGAATGCTGAGGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGC----AGAC 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 GACCTGATGTCT----GCTGGGCAATCTTGCACATGAGATGTGGCTGGTCCGACCTCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                          APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427032
CURRENT APPLICATION NUMBER: US/11/344,932
CURRENT FILING DATE: 2006-02-01
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64.5%; Pred. No. 6.7e-18;
cive 0; Mismatches 80
                                                                   MCNeil, Patricia D.
Houghton, Raymond L.
Vinals y de Bassols, Carlota
                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2006-02-01
PRIOR FILING DATE: 2002-05-09
PRIOR FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: 10/1012,896
PRIOR APPLICATION NUMBER: 09/895,814
PRIOR APPLICATION NUMBER: 09/895,814
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-09
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-02-09
PRIOR PELING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/799,143
PRIOR FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/799,143
PRIOR FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 09/695,166
PRIOR PELING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-10-07
PRIOR FILING DATE: 2000-10-07
PRIOR FILING DATE: 2000-10-07
PRIOR FILING DATE: 2000-00-02
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                                                                                                                                                 Foy, Teresa M.
Watanabe, Yoshihiro
Meagher, Madeleine Joy
Yasir A. W. William T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 64.5
Matches 160; Conservative
                                                     John
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ORGANISM: Homo sapiens
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                                                                                                                   APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFRENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 89.2; DB 8; Length 5
Pred. No. 5e-19;
0; Mismatches 28; Indels
                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR PILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
                     Sequence 32477, Application US/11266748A
Publication No. US20060134663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/700,293 PRIOR FILING DATE: 2005-07-18 SEQ ID NOS: 483996 SOFTWARE: Patentin version 3.3
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Publication No. US20060269532A1
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Falos, Michael D.
APPLICANT: Ranger, Gary R.
APPLICANT: Retter, Marc W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.2%;
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Day, Craig H.
Vedvick, Thomas S
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.29
Best Local Similarity 79.1<sup>3</sup>
Matches 106; Conservative
                                                Publication No. US200601:
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Samuel X
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US-11-266-748A-32477
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US-11-344-932-67/c
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LENGTH: 5449
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SOFTWARE: Pater
SEQ ID NO 58517
LENGTH: 15439
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                CURRERAL INFORMATION:

APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.

ITILE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND
ITILE OF INVENTION: METHODS FOR THEIR USE
FILE REFERENCE: 21002-1.4287
CURRENT APPLICATION NUMBER: US/11/349,541
CURRENT APPLICATION NUMBER: US 09/116,134
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-07-14
PRIOR FILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-09
PRIOR PILING DATE: 1998-02-09
PRIOR PILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/904,809
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/806,596
PRIOR FILING DATE: 1997-08-01
PRIOR FILING DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/806,596
PRIOR FILING DATE: 1997-08-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291 haaggagriccreagaccagccccarcrcargriccaagacreccagccrcraaag 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 ATCAGGTCTCAGAGGAGAACTCTCTCAAAAGTGAATCTCCCAGCACAGCACAGCTGCTCTA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 CACAATCGTGGCTAGACTTCTTTTAAGCAAGTCCCCTTTTTTAAAAGGGGAACTCTCA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 GACCTGATCTTTAGAGGCTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGC 283
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Sequence 46, Application US/10669920
Publication No. US20060194265A1
Sequence 100 No. US20060194265A1
Septicant No. US20060194265A1
APPLICANT: Moriation David W.
APPLICANT: Malandro, Marc S.
FILE OF INVENTION: NOVEL THERABEUTIC TARGETS IN CANCER
FILE REFERENCE: 20366-066001
CURRENT FILING DATE: 2036-06601
FRICH APPLICATION NUMBER: US 10/064,113
PRIOR FILING DATE: 2001-10-23
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-08
PRIOR FILING DATE: 2001-11-30
PRIOR PLICATION NUMBER: US 10/034,650
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2001-11-20
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-10-30
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-10-30
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Pred. No. 6.7e-18;
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Best Local Similarity 64.5
Matches 160; Conservative
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CORGANISM: Homo sapien
US-11-349-541-67
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 TCTCCCAGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.5%; Score 75.2; DB 8; Length 154394; larity 82.7%; Pred. No. 1.6e-13; Conservative 0; Mismatches 18; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Rarl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPRENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 10/322,281
PRIOR FILING DATE: 2002-12-17
PRIOR PILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 1441
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 46
LENGTH: 25694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR PELING DATE: 2005-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
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                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)...(25694)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 79.8
Matches 91; Conservative
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US-11-266-748A-58517
                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
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Best Local Similarity
Matches 86; Conserv
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Search completed: December 31, 2006, 19:49:14 Job time : 139.37 secs

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LENGTH: 385
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| FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US08_PUBCOMB.seq:*
| FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US08_PUBCOMB.seq:*
| FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US09_PUBCOMB.seq:*
| FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US09_PUBCOMB.seq:*
| FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US10_PUBCOMB.seq:*
| FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US11A_PUBCOMB.seq:*
| FBMC_Celerra_SIDS3/ptodate3/2/pubpna/US11B_PUBCOMB.seq:*
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7716.790 Million cell updates/sec
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Sequence 11258,
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                                                                                                                                                  December 31, 2006, 12:22:01 ; Search time 613.045 Seconds
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Sequence 67,
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Sequence 67,
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-198-846-11258
US-11-234-786-701
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US-09-780-669-67
US-09-822-827-67
US-09-115-453-67
US-09-895-814-67
US-10-112-896-67
US-10-144-6788-67
US-10-294-025-67
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                                                                                               - nucleic search, using sw model
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Maximum Match 100%
Listing first, 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length
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        307.2
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        3 US-09-759-143-701
        Sequence 701, App Sequence
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ALIGNMENTS

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Sequence 67, Application US/09759143

Patent No. US2002002248A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitchan, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Marc M.
APPLICANT: Harlocker, Marc M.
APPLICANT: Harlocker, Marc M.
APPLICANT: Reter, Marc M.
APPLICANT: Reter, Marc M.
APPLICANT: Reter, Marc M.
APPLICANT: Reter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Stolk, Yasir A.W.
APPLICANT: Stolk, Yasir A.W.
APPLICANT: Wang, Aljun
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aljun
APPLICANT: Wall APPLICATION NUMBER: US/09/759,143
CURRENT APPLICANT: Wang, Wall APPLICANT: Wang, Walch
ACCANISM: Homo sapien

JUDG, 04, Fred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0; Indels 0; Gaps
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1 ACTACACACACTCCCACTTGCCCTTGTGAGACACTTTGTCCCCAGCACTTTAGGAATGCTGA 60

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us-09-232-880-67.rnpbm

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301 CCTCTCCCAGGGCCCCAGCCTGGCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
                                  61 GGTCGGACCAGCACACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC 120
                                                                                                          241 CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
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                                                                                     CCCTTTTAAAAAAGGGGACTTGCTTAAAAAAGAAGTCTAGCCACGATTGTGTAGAGCAGC 180
                                                                                                                                                                                                                                                         241 CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG
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Best Local Similarity 100.0%;
Matches 385; Conservative 0
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TELEFAX: (206) 682-6031
INFORMATION FOR SEO ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 385 base pairs
TYPE: nucleic acid
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STRANDEDNESS:
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US-09-030-606-67
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                                                                            GGTCGGACCACACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGATTC
                                                                                                                             CCCTTTTAAAAAAGGGGACTTGCTTAAAAAAAGAAGTCTAGCCACGATTGTGTAGAGCAGC
                                                                                                                                                                                                                           ACTACACACACACTCCCACTTGCCCTTGTGAGACACTTTGTTCCCCAGCACTTTAGGAATGCTGA
GGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC
                                                                                                                                                  TGTGCTGTGCTGGAGATTCACTTTTGAGAGATTCTCCTCTGAGACCTGATCTTTAGAGG
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APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
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Vedvick, Thomas S.
Carter, Darrick
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ORGANISM: Homo sapien
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Sequence 67. Application US/09030606
| Patent No. US20020081580A1
| GENERAL INFORMATION:
| APPLICANT: Xu, Jiangchun |
| APPLICANT: Dillon, Davin C. |
| TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS IS NUMBER OF SEQUENCES: 224 |
| CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: SEED and BERRY LLP |
| STRET: 6300 Columbia Center, 701 Fifth Avenue |
| CITY: Seattle |
| STATE: WA |
| COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: DatentIn Release #1.0, Version #1.30
SUSTYARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,606
FILING DATE: 25-FEB-1998
CLASSIFICATION:
NAME: Mark, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C3
TELECOMMUNICATION INFORMATION:
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301 CCTCTCCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
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Patent No. US20020090372Al
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: MCTHODE FOR IMMUNOTHERAPY OF PROSTATE CANCER AND
TITLE OF INVENTION: COMPOUNDS FOR THEIR USE
FILE REPERENCE: 210121.427C4
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 3.0
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Publication No. US20020182596A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun C.
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
ITTLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REPERENCE: 210121.428C6
CURRENT APPLICATION NUMBER: US/09/232,880
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Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0;
                                                                                 361 CATAGTTTCTGTGCTAGTGGACCGT 385
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ORGANISM: Homo sapien
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US-09-115-453-67
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US-09-232-880-67
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                                                                                                     TGTGCTGTGCTGGAGATTCACTTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG
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                            ACTACACACACTCCACTTGCCCTTGTGAGACACTTTGTCCCCACCTTTAGGAATGCTGA
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SEQ ID NO 67
LENGTH: 385
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100.0%; Score 385; DB 3; L
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0;
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Patent No. US20020081680A1
GENERAL INFORMATION:
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ORGANISM: Homo sapien
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C25
CURRENT APPLICATION NUMBER: US/09/895,814
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                                                                                                                                                                                  100.0%; Score 385; DB 3; Length 385; 100.0%; Pred. No. 2.2e-126;
                                                                                                                                                                                                                          0; Mismatches
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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; Sequence 67, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
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Hepler, William T.
Henderson, Robert A.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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                                                                                                       type: DNA CORGANISM: Homo sapien US-09-895-793-67
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Best Local Similarity
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
                                                                                                                                                                                      100.0%; Score 385; DB 3; Length 385; 100.0%; Pred. No. 2.2e-126; ive 0; Mismatches 0; Indels (
  CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
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CURRENT APPLICATION NUMBER: US/09/895,793
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Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020192763A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: XU, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Day, Craig H.
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Skeiky, Yasir A.W.
Hepler, William T.
                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 385; Conservative
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                                                                                                           TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 7
US-09-895-793-67
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APPLICANT:
APPLICANT:
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61 GGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC 120
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APPLICANT: Fanger, Gary
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                     100.0%; Score 385; DB 6; L
100.0%; Pred. No. 2.2e-126;
tive 0; Mismatches 0;
                  CURRENT APPLICATION NUMBER: US/10/012,896 CURRENT FILING DATE: 2001-12-10 NUMBER OF SEQ ID NOS: 1011 SOFTWARE: PastSEQ for Windows Version 3.0
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
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CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 CATAGTTTCTGTGCTAGTGGACCGT 385
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No. US20030088062A1
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
FILE REFERENCE: 210121.427C27
                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 385; Conservative
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Reed, Steven G.
                                                                                                                                                                     ORGANISM: Homo sapiens
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CORGANISM: Homo sapien
US-10-010-940-67
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US-10-010-940-67
                                                                                                        SEQ ID NO 67
LENGTH: 385
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APPLICANT:
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APPLICANT: Mantanabe, Yoshihiro
APPLICANT: Maagher, Madeleine Joy
APPLICANT: CAMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                              Length 385;
                                                                                                                                                                                                                                                                                   1 ACTACACACACTCCACTTGCCCTTGTGAGACACTTTGTCCCAGCACTT
                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                            100.0%; Score 385; DB 3; L
ilarity 100.0%; Pred. No. 2.2e-126;
Conservative 0; Mismatches 0;
                  NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Ralos, Michael D.
APPLICANT: Retter, Marc M.
APPLICANT: Stolk, John A.
2001-06-29
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Hepler, William T.
Henderson, Robert A.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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                                                                                                      TYPE: DNA
CORGANISM: Homo sapien
US-09-895-814-67
CURRENT FILING DATE:
                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 385; Conserv
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US-10-012-896-67
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100.0%; Pred. No. 2.2e-126;
ive 0; Mismatches 0;
                               100.0%; Score 385; DB 7; I 100.0%; Pred. No. 2.2e-126;
                                                                  0; Mismatches
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ORGANISM: Homo sapiens
US-10-294-025-67
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US-10-144-678A-67
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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Length 385;
                                   Indels
100.0%; Score 385; DB 6; I
100.0%; Pred. No. 2.2e-126;
ive 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
TYPE: DNA
ORGANISM: Homo sapiens
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Skeiky, Yaair A. W.
Hepler, William T.
Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals y de Bassols, Carlota
Foy, Teresa M.
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US-10-144-678A-67
US-10-144-678A-67
; Sequence 67, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Garter, Marc W.
APPLICANT: Garter, Thomas S.
APPLICANT: Carter, Darrick
Query Match 100.
Best Local Similarity 100.
Matches 385; Conservative
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Publication No. US20040141989A1

GENERAL INFORMATION:

APPLICANT: Vu. Jiangchun

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 21011.42794

CURRENT APPLICATION NUMBER: US/10/688,838

CURRENT FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 228

SOFTWARE: PSETSEQ for Windows Version 4.0

SEQ ID NOS: 228
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US-11-234-786-67
; Sequence 67, Application US/11234786
; Publication No. US20060024301A1
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Matches 385; Conservative
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; ORGANISM: Homo sapiens
US-10-688-838-67
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US-10-688-838-67
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Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqin
Reed, Steven G.
Kalos, Michael D.
                                                                                                                               Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
                                                                                         Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Matches 385; Conservative
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APPLICANT:
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241 CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
                                                         101 CCTCTCCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
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US-10-294-025-1036
US-10-294-025-1036
US-10-294-025-1036
Sequence 1036, Application US/10294025
Publication No. US20030185830A1
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210.12.427C29
CURRENT APPLICATION NUMBER: US/10/294,025
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 1038
SEQ ID NO 1036
LENGTH: 3710
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99.2%; Score 381.8; DB 7; Length 3710;
Best Local Similarity 99.5%; Pred. No. 8.4e-125;
Matches 383; Conservative 0; Mismatches 2; Indels 0;
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CORGANISM: Homo sapiens
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US-09-020-956-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   **EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*

**EMC_Celerra_SIDS3/ptodata/2/ina/5_COMB.seq:*

**EMC_Celerra_SIDS3/ptodata/2/ina/6_COMB.seq:*

**EMC_Celerra_SIDS3/ptodata/2/ina/R_COMB.seq:*

**EMC_Celerra_SIDS3/ptodata/2/ina/T_COMB.seq:*

**EMC_Celerra_SIDS3/ptodata/2/ina/T_COMB.seq:*

**EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*

**EMC_Celerra_SIDS3/ptodata/2/ina/PCTUMB.seq:*

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                       GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-679-426-701
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US-09-352-616A-67

US-09-232-149A-67

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US-09-636-215-67

US-09-685-166A-67

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                                                                                                                     - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Sequence 67, Application US/09020956

Patent No. 6261562

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: APPLICANT: Xu, Jiangchun
APPLICANT: Xu, A
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APPLICATION NUMBER: US/09/020,956 FILING DATE: 09-FEB-1998 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 385; DB 3; I
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0;
                 US-10-012-896-701

US-10-144-678A-701

US-09-636-115-700

US-09-639-126-700

US-09-659-126-700

US-09-659-126-700

US-09-651-236-700

US-10-012-896-700

US-10-012-896-700

US-10-144-678A-700

US-09-020-956-67

US-09-352-616A-67

US-09-352-616A-67

US-09-352-616A-67

US-09-352-616A-67

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US-09-352-616A-67

US-09-368-489-67
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US-09-679-426-67
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 385 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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  Length 385;
                                          Indels
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APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Read, Steven G.
APPLICANT: Reads, Michael
APPLICANT: Fanger, Gary
APPLICANT: Farter, Mark
APPLICANT: Solk, John
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FRASESO for Windows Version 3.0
; Score 385; DB 3; 1; Pred. No. 5.9e-124; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 CATAGTTTCTGTGCTAGTGGACCGT 385
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 67, Application US/09439313; Patent No. 6329505; GENERAL INFORMATION:
      100.0%;
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    Query Match
Best Local Similarity 100.
Matches 385; Conservative
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CORGANISM: Homo sapien
US-09-439-313-67
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Best Local Similarity
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US-09-439-313-67
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LENGTH: 385
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Patent No. 6262245

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS INTOMERS OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                   240
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 CATAGITICIGIGCIAGIGGACCGI 385
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
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US-09-030-607-67
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Patent No. 6613872
GENERAL INPORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION NUMBER: US/09/159,812A
CURRENT APPLICATION NUMBER: US/09/159,812A
CURRENT FILING DATE: 1998-09-23
NUMBER OF 'SEQ ID NOS: 306
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 385;
                                                                                                                                                                                                                 APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Micham, Jeanin C.
APPLICANT: Micham, Jennifer Lynn
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.42706
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT APPLICATION NUMBER: US/09/232,149A
SOFTWARE: FESTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 385; DB 3; Length 3
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels
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; Patent No. 6465611
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LENGTH: 385
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Fatent No. 639528
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Jiang, Yuqui
APPLICANT: Jiang, Yuqui
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.427C8
CURRENT PELLING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SEQ ID NO 67
LENGTH: 385
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Best Local Similarity 100.
Matches 385; Conservative
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ORGANISM: Homo sapien
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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ORGANISM: Homo sapien
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT APPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
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                                                                                     Length 385;
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                                                                                    Query Match 100.0%; Score 385; DB 3; L Best Local Similarity 100.0%; Pred. No. 5.9e-124; Matches 385; Conservative 0; Mismatches 0;
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Patent No. 662092.
APPLICANT: Xu, Jiangchun APPLICANT: Xu, Jiangchun APPLICANT: Mitcham, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
           ; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-159-812-67
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CRGANISM: Homo sapien
US-09-636-215-67
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100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.0%; Score 385; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0; Indels
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APPLICANT Henderson, Robert A.
APPLICANT Henderson, Robert A.
APPLICANT Fanger, Gary R.
APPLICANT Fanger, Gary R.
APPLICANT Setter, Marc W.
APPLICANT Boy, Craig H.
APPLICANT Day, Craig H.
APPLICANT Day, Yang S.
APPLICANT Li, Samuel
APPLICANT Wang, Ajun
APPLICANT Seckley, Yasir A.W.
APPLICANT Wang, Ajun
APPLICANT Booker William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE FASTERO FOR Windows Version 3.0
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CCTCTCCCAGGGCCCCAGCCTGGCCACCCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
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                                                                                                                                                                                                                            Sequence 67, Application US/09688489
; Sequence 67, Application US/09688489
; Patent No. 666437
; GENERAL INFORMATION:
   APPLICANT: Dillon, Davin C.
   APPLICANT: Dillon, Davin C.
   APPLICANT: Mitcham, Jennifer Lynn
   TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
   TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
   FILE REFERENCE: 210121.427D2
   CURRENT APPLICATION NUMBER: US/09/688,489
   CURRENT APPLICATION NUMBER: US/09/688,489
   NUMBER OF SEQ ID NOS: 338
   NUMBER OF SEQ ID NOS: 338
   SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0;
                                                                                                           361 CATAGTTTCTGTGCTAGTGGACCGT 385
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Patent No. 6755515
GENERAL INPORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
                                                                                     361 CATAGITICIGIGCIAGIGGACCGI
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GORGANISM: Homo sapien
US-09-688-489-67
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US-09-688-489-67
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SEQ ID NO 67
LENGTH: 385
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US-09-679-426-67
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Patent No. 6657056
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Ujllon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND TITLE OF INVENTION: METHODS FOR THEIR USE FILE REPERENCE: 210121.427C4
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT PILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 100.0%; Pred. No. 5.9e-124;
Matches 385; Conservative 0; Mismatches 0;
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US-09-115-453-67
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US-09-115-453-67
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                                                                              APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121-427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Setter, Marc W.
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
Wang, Aijun
  Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Best Local Similarity 100.
Matches 385; Conservative
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CORGANISM: Homo sapien
US-09-759-143-67
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APPLICANT:
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APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reter.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Overick, Thomas S.
APPLICANT: Darrick
APPLICANT: Overick, Thomas S.
APPLICANT: Wang, Aljun
APPLICANT
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US-09-759-143-67
Sequence 67, Application US/09759143
Patent No. 6800746
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
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Best Local Similarity 100.0
Matches 385; Conservative
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; ORGANISM: Homo sapien
US-09-679-426-67
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100.0%; Pred. No. 5.9e-124;
vative 0; Mismatches 0; Indels
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; Sequence 67, Application US/09657279
; Patent No. 6894146
                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
INFORMATION: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 Base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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ATTORNEY/AGENT INFORMATION:
                               NAME: Maki, David J.
REGISTRATION NUMBER: 31,
REFERENCE/DOCKET NUMBER:
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Vedvick, Thomas S
Carter, Darrick
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Dillon, Davin C.
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Hepler, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches -385; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-030-606-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT:
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APPLICANT: Xu, Jiangchun

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                        APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.42718C18
CURRENT PELLING NUMBER: US/09/651,236
CURRENT FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 865
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,606
FILING DATE: 25-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 385; DB 3; L. Best Local Similarity 100.0%; Pred. No. 5.9e-124; Matches 385; Conservative 0; Mismatches 0;
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Patent No. 6887660
Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-651-236-67
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APPLICANT:
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; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND FILE REPERENCE: 210121.427C19
; FILE REPERENCE: 210121.427C19
; CURRENT APPLICATION WHERE: USO9/657,279
; CURRENT PAPLICATION WHERE: 2000-09-06
; NUMBER OF SEQ ID NOS: 877
; SEQ ID NO 67
; LENGTH: 385
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-657-279-67
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Search completed: December 31, 2006, 12:31:10 Job time : 90.8616 secs

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ACN87074 Breast ca ACN84137 Breast ca Abv26126 Human pro Abv27659 Human pro Abv21835 Human pro

Acn90279 Breast ca Aal14082 Human bre Acn81332 Breast ca Aal15514 Human bre Aal24358 Human bre Acn85503 Breast ca Acn91316 Breast ca

alli453 Human bre Acn81654 Breast ca Aal18756 Human bre Aal20352 Human bre Aal11453 Human bre

Minimum DB seq Maximum DB seq

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Database

Scoring table:

Searched:

Perfect score:

Sequence:

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This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as
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   Xu J, Dillon DC;
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8969.963 Million cell updates/sec
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                GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
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Claim 12; Page 61; 130pp; English
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encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, amintor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate cancers. (Updated on 25-MAR-2003 to correct PR field.)
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Pred. No. 1.8e-117;
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The present sequence is a DNA which encodes an immunogenic portion of a prostate tumour protein. The encoded immunogen, or the DNA itself, can be used as a vaccine for the treatment of prostate cancer. The DNA was identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library
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Homo sapiens.
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                                                                                                                                                     The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polymucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polypeptides and polypeptides and in gene therapy. The polypeptides and polypeptides comprising them can be used for inhibiting the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or antibodies for passive immuno therapy. A portion of the polypublicate can be used as a probe or to modulate the expression of the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAA06241 to AAA06691 and AAX82000 to AAX82000 represent sequences used in the exemplification of
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prostate cancer; cytostatic; vaccine; ss.
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                                                                                       New polypeptide useful for treating and diagnosing prostate comprises an immunogenic portion of prostate tumor protein.
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The present invention relates to a new polypeptide comprising an immunogenic portion of a prostate protein. The invention is useful for inhibiting the development of prostate cancer in a patient. The invention is also useful as markers for diagnosing prostate cancer and for monitoring diseases progression in patients. The present nucleic acid sequence represents a DNA sequence that is part of a gene encoding a human prostate tumour protein
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97US-00904804.
98US-00020956.
98US-00030607.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated reprepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH931357 to AAH931944 and AAM01115 to AAM01318 represent
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                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG
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Retter MW, Stolk JA, Skeiky YAW;
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0
                                                                                          Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
                                                               Human prostate-specific cDNA sequence P80 (also P740P)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 100.0%; Score 385; DB 4; L
Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 250; 543pp; English
                                                                                                                                                                                                                                                                                                                                           Xu J, Dillon DC, Mitcham JL,
Kalos MD, Fanger GR, Day CH,
Wang A, Meagher MJ;
                                                                                                                                                                                                                                               16-JAN-2001; 2001WO-US001574.
                                                                                                                                                                                                                                                                              14-JAN-2000; 2000US-00483672
                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the present invention
                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP.
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                                                                                                                                                                                WO200151633-A2
                                                                                                                                               Homo sapiens.
                                04-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vaccines.
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301 CCTCTCCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer.
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Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
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A, Day CH, Vedvick TS,
spler WT, Henderson RA;
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100.0%; Pred. No. 1.8e-117;
iive 0; Mismatches 0;
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                                                                                                                        CATAGTTTCTGTGCTAGTGGACCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate cDNA sequence #67.
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2000US-00593793.
2000US-00695783.
2000US-00636215.
2000US-00631236.
2000US-00657279.
                                                                                                                                                                                                                                                                                                            AAS63515 standard; cDNA; 385
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Matches 385; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have cytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polymucleotides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonucleotides that hybridise to a polymucleotide that encodes a prostate specific protein are useful for detecting the
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                                                                                                      GGTCGGACCAGCCACATCTCCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC 120
                                                                                                                                                                                          CCCTTTTAAAAAAGGGGACTTGCTTAAAAAAGAGTCTAGCCACGATTGTGTAGAGCAGC 180
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                                        TGTGCTGTGCTGGAGATCACTTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG
                                                                                                                                 GGTCGGACCACACTCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC
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                    ACTACACACACTCCACTTGCCCTTGTGAGACACTTTGTCCCAGCACTTTAGGAATGCTGA
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prostate cancer;
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presence or absence of a cancer or monitoring the progression progression of a cancer, especially prostate cancer. AAH02422 AAB74798 to AAB74821 and AAB74830 are sequences used in the
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                                                                                                                                                           Length 385;
                                                                                                                                                                                                    0; Indels
                                                                                                            Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
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, Day CH, Skeiky YAW,
                                                                                                                                                    Query Match 100.0%; Score 385; DB 4; I Best Local Similarity 100.0%; Pred. No. 1.8e-117; Matches 385; Conservative 0; Mismatches 0;
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                                                                  exemplification of the present invention
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4D, Retter
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18-NOV-1999;
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                                                          The present invention describes an isolated polypeptide (PI) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polymcleotides (NI) encoding (PI). (PI) and (NI) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P77P and B105D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region.

Prostate specific antigan (PSA) P51S was located on chromosome 1.

AAH84671 to AAH85143 and AA989000 to AAG99077 represent polymucleotide and polypeptide sequences used in the exemplification of the present
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prostate-specific protein, useful in the diagnosis and therapy prostate cancer.
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                                                                                                                                                                                                                                  Length 385;
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                                                                                                                                                                                        Polypeptide comprising part of the Wilms Tumor gene product sequence is used in the diagnosis and treatment of malignant diseases e.g. leukemia and cancer associated with WII.
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Matches 385; Conservative
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09-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prostate specific protein and its encoding polynucleotide, useful for the
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Carter D;
Hural J;
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0; Mismatches 0; Indels 0
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Best Local Similarity 100.0%;
Matches 385; Conservative 0;
                                                                                 29-JUN-2001; 2001US-00895793.
                                                                                                       04-OCT-1999; 99US-0157455P.
04-OCT-2000; 2000US-00679272.
28-MAR-2001; 2001US-00822827.
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MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C
FOY T M.
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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MITCHAM J L.
HARLOCKER S I
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DAY C H.
VEDVICK T S.
CARTER D.
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                                                                                                                                                                                                      JIANG Y.
                                   US2002192763-A1
                Homo sapiens.
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                                                                                                                                                                                                                                          (RETT/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel polynucleotide encoding polypeptide comprising a portion of prostate tumor protein useful for inhibiting development of prostate cancer or for treating prostate cancer in a patient.
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                                                                                                                                                                                                                                Human; prostate tumour protein; prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
100.0%; Score 385; DB 5; L
Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0;
                                                                                                                                                                      Human prostate tumour cDNA P86 #4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Col 81; 105pp; English.
AAS10066 standard; cDNA; 385 BP
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97US-00904804.
98US-00020956.
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Best Local S
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61 GGTCGGACCACCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC 120

1 ACTACACACTCCACTTGCCCTTGTGAGACACTTTGTCCCAGCACTTTAGGAATGCTGA

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241 CTGGGCAGTCTTGCACATGAGATGGGCCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300 241 CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCACTTG 300
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                                                                                                                                                                                                                                                                                                                         The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCTTTTAAAAAAGGGGACTTGCTTAAAAAGAAGTCTAGCCACGATTGTGTAGAGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTGCTGTGCTGGAGATTCACTTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG
                                                                                                                                                                                Kalos MD;
Carter D;
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for the
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 385; DB 6; Length 385; Best Local Similarity 100.0%; Pred. No. 1.8e-117; Matches 385; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                     New prostate-specific polynucleotides for diagnosing and diseases, in particular prostate cancer, and as markers f progression of cancer.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 385 BP; 86 A; 105 C; 94 G; 100 T; 0 U; 0 Other;
                                                                                                                                                                               Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATAGTTTCTGTGCTAGTGGACCGT 385
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                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 67; 87pp; English.
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                                                       STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
                                                                                                                                                        HENDERSON R A.
HARLOCKER S
        JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                                                               WPI; 2002-255649/30.
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Fanger G
Li SX,
        (JIAN/)
(KALO/)
(FANG/)
                                                          (STOL/)
(DAYC/)
(VEDV/)
(CART/)
(LISX/)
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                                                                                                                                                                                                                     CTCTCCCAGGCCCCAGCCTGCCTACAGGCCACTCTCAGATGCCCATAC 360
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                                                                                                                         TGTGCTGTGCTGGAGATTCACTTTTGAGAGATTCTCCTCTGAGACCTGATCTTTAGAGG
                                                                                                                                                                       CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG
                                                                                                                                                                                                         CCTCTCCCAGGGCCCCAGGCCTGGCTTACAGGGCACTCTCAGATGCCCATAC
            GGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC
                                                                                                           TGTGCTGTGCTGGAGATTCACTTTTGAGAGATTCTCCTCTGAGACCTGATCTTTAGAGG
                                                                                                                                                          CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
                                                                                                                                                                                                                                                                      CATAGTTTCTGTGCTAGTGGACCGT 385
                                                                                                                                                                                                                                                        CATAGITICIGIGCTAGIGGACCGI 385
                                                                                                                                                                                                                                                                                                                                                                                                                     Human P80 cDNA sequence SEQ ID NO 67.
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01-AUG-1997; 97US-00020956.
25-FEB-1998; 98US-00020956.
14-JUL-1998; 98US-00115453.
15-JAN-1999; 99US-00158112.
15-JAN-1999; 99US-00232149.
09-APR-1999; 99US-0048946.
11-JUL-1999; 99US-00438418.
11-JUL-1999; 99US-00443686.
14-JAN-2000; 2000US-00561100.
12-MAY-2000; 2000US-00561100.
12-MAY-2000; 2000US-00567737.
13-JUN-2000; 2000US-00567737.
10-AUG-2000; 2000US-00567737.
10-AUG-2000; 2000US-00567737.
10-AUG-2000; 2000US-00567737.
10-AUG-2000; 2000US-00567737.
10-AUG-2000; 2000US-00567737.
10-AUG-2000; 2000US-00567737.
                                                                                                                                                                                                                                                                                                                                            ABL94887 standard; cDNA; 385
                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; gene; ss.
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DILLON D C.
MITCHAM J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US2002022248-A1
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The present invention relates to novel prostate-specific proteins (PSP) and their coding sequences. The PSPs and their coding sequences are useful for stimulating an immune response in a patient, or for treating prostate cancer in a patient and for determining, detecting or diagnosing the presence of a cancer in a patient. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New prostate-specific proteins and genes, useful in gene therapy, particularly for stimulating an immune response in a patient, or treating prostate cancer in a patient, as well as for diagnosing prostate cancer
301 CCTCTCCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA, MD, Panger GR, Vedvick TS; D. Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J; D. Houghton RL, Vinals Y De BassolsC, Poy TM, Watanabe Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTACACACACTCCCACTTGCCCTTGTGAGACACTTTGTCCCCAGCACTTTAGGAATGCTGA
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                                                                                                                                                                                                                                                                                                                                                       prostate-specific protein; PSP; human; cancer; ss.
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Best Local Similarity 100.0%; Pred. No. 1.8e-117;
Matches 385; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                              Prostate tumour specific cDNA sequence SEQ ID 67.
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                                             CATAGTTTCTGTGCTAGTGGACCGT
                                                                                                                                                                                        ВР
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29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
                                                                                                                                                                                      ACC95051 Btandard; cDNA; 385
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                                                                                                                                                                                                                                                                                                                                                       therapy;
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Carter D, Li
Mcneill PD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method of detecting prostate cancer by contacting a biological sample from a patient with: (a) a binding agent that binds to a polypeptide having an immunogenic portion of a prostate protein or its variant; (b) 2 oligonucleotide primers, where 1 of the oligonucleotides is specific for a DNA encoding the polypeptide of (a); or (c) an oligonucleotide probe specific for a DNA molecule encoding the polypeptide of (a). The method and polypeptides are useful for diagnosing, treating, particularly by immunotherapy, monitoring the progression, and inhibiting the development of prostate cancer in a patient. The polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. ABSSB350-ABSSB346 represent human prostate tumour CDNA sequences of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting prostate cancer comprises contacting a sample with an agent capable of binding to a polypeptide with an immunogenic portion of a prostate protein, oligonucleotide primers or a probe specific for DNA encoding the polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTACACACACTCCCACTTGCCCTTGTGAGACACTTTGTCCCCAGCACTTTAGGAATGCTGA
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                                                                                 tumour; immunotherapy; prostate cancer; gene;
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Pred. No. 1.8e-117;
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97US-00904809.
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                                          tumour cDNA
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98US-00115412.
99US-001521149.
99US-0028946.
99US-0028946.
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2001US-00012896.
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09-APR-1999;
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100.0%; Score 385; DB 10; Length 385; 100.0%; Pred. No. 1.8e-117; tive 0; Mismatches 0; Indels 0

Best Local Similarity 100. Matches 385; Conservative

Query Match

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121 cccrititaaaaaagggacingcinaaaaagaagiciagccacgarigigiagagcagc 180

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TGTGCTGTGCTGGAGATTCACTTTTGAGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG

CTGGGGAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG

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XX WPI, 2003-756193/71.

XX Wer, 2003-756193/71.

XX New isolated polypeptide for use in a vaccine for stimulating an immune response, or for treating or diagnosis cancer, preferably prostate are response, or for treating or diagnosis cancer, preferably prostate are response, or for treating or diagnosis cancer, preferably prostate are response, or for treating or diagnosis cancer, preferably prostate expenses of ADB13563 comprising a sequence ADB1487. The cancer is leaded and poptides concain naturally processed peptides comprise a fragment ADB13563 of that contain naturally processed constant and peptides encoded by a human prostate specific configurable proteins and applyable encoded by a human prostate specific configurable proteins and applyable encoded by a human prostate specific configurable proteins and applyable state of the proteins and peptides, expression vectors, a host cell cransformed with the vector, an isolated art builds to the protein or peptides detecting the annual to a binding agent that binds to the protein or peptides detecting transment that specifically binds to the protein or peptide detecting the annual of configurable that binds to the appendence of a cancer in a patient to presence of an annual to peptides or proteins; similaring contacting or expanding or expanding cluster of differentiation (Comprising contacting or expanding or expanding cluster of differentiation (COM+) and admining the peptides or proteins; similaring the peptides or proteins; similaring the peptides or proteins are presented or cancer in a patient and treating prostate cancer in a patient of differentiation (COM+) and demining cells express the peptides or the apprides or antigen presenting cluster of differentiation (COM+) and demining cells express the peptides or antigen presenting cells concer in a patient. The peptides, nucleic acids antibodes or cancer in a patient. The peptides or antigen presented or cancer in a patient. The peptides or antigen presented or cancer in a patient. The peptides or antige
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PP 25-FEB-1998 JP 1998537008
PR 25-FEB-1998 JP 1998537008
PR 25-FEB-1999 US 08/904809 PR 25-FEB-1999 US 09/020747
DI JIANGCHUN XU,DAVIN C DILLON
PC GOIN33/574, GOIN33/577, CO7K16/30, A61K39/395, A61K47/48, C12Q1/68, PC GOIN33/573, Eingle;
CC Topology: Linear;
CC Topology: Linear;
CC Topology: Linear;
CC Compounds for immunodiagnosis of prostate cancer and methods CC Topology: Linear;
CC Compounds for immunodiagnosis of prostate cancer and methods FH Key Location/Qualifiers
FH Key Location/Qualifiers
FT Source (human)'.
                                                                                                                                                                                                                                                                                                                                                                                                                              385 bp DNA linear PAT 27-AUG-2002 for immunodiagnosis of prostate cancer and methods for
           AX200437 Sequence
AX267093 Sequence
AX367093 Sequence
AX38952 Homo sapi
AL512624 Human chr
AL512624 Human chr
AL512624 Human chr
AC122619 Homo sapi
AC124149 Pan trogl
BV575629 G5916674
AC123981 Pan trogl
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AC182114 Pan trogl
AC18214 Pan trogl
AC18215 Pan trogl
AC182395 Pan trogl
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 385)
Xu, J. and Dillon, D.C.
Compounds for immunodiagnosis of prostate cancer and
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CORIXA CORP
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/mol_type="genomic DNA"
/db_xref="taxon:9606"

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JP 201513886-A/67
04-SEP-2016
25-FEB-1998 JP 1998537008
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AC124149
BV575629
AC123981
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AC093838
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CNS07EED
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Homo sapiens (human)
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(c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
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                   sapiens (human)'
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Xu,J., Dillon,D.C. and Mitcham,J.L.
Compounds for immunotherapy of prostate
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                     /organism='Homo
Location/Qualifiers
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Patent: US 6465611-A 67 15-OCT-2002;
Corixa Corporation; Seattle, WA
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/wol_type="genomic DNA"
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Sequence 67 from patent US 64
AR237163
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Matches 385; Conservative
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OCH Homo sapiens (human)

PN JP 2002520054-A/67

PN JP 2002520054-A/67

PD 09-JUL-1999 US 09/115453,14-JUL-1998 US 09/116134 PR

14-JUL-1999 US 09/52820,13-SEP-1998 US 09/232149 PR

15-JAN-1999 US 09/232880,15-JAN-1999 US 09/232149 PR

15-JAN-1999 US 09/232880,15-JAN-1999 US 09/232149 PR

15-JAN-1999 US 09/23880,15-JAN-1999 US 09/232149 PR

15-JAN-1999 US 09/2388946

PI JANGCHUN XU,

PI JENNIFER LYNN MITCHAM

PC CILNIS/O9, AGIK39/00,AGIK39/395,CO7K14/47,CO7K16/30,

PC CILNIS/10,

PC CINNIS/10,

PC COMPOUNDER CINNIS/10,

PC CI
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1 (bases 1 to 38s)
Dillon, D.C., Harlocker, S.L., Yuqiu, J., Xu, J. and Mitcham, J.L.
Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use
Patent: JP 2002520054-A 67 09-JUL-2002;
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                        Length 385;
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                        100.0%; Score 385; DB 2; Length 3 100.0%; Pred. No. 3.8e-117; ive 0; Mismatches 0; Indels
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JP 2002520054-A/67.
Homo sapiens (human)
Homo sapiens
                          Query Match
Best Local Similarity 100.
Matches 385; Conservative
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                  301 CCTCTCCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yuqiu,J.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and
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Matches 385; Conservative 0; Mismatches 0;
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Sequence 67 from patent US 6329505.
AR366883.1 GI:34599858
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Sequence 67 from patent US 6395278.
AR370779 AR370779.1 GI:34607672
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/mol_type="genomic DNA"
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Unclassified.
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Xu,J., Dillon,D.C., Mitcher,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
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Best Local Similarity 100.0%; Pred. No. 3.8e-117;
Matches 385; Conservative 0; Mismatches 0;
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Corixa Corporation, Seattle, WA
Location/Qualifiers
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    .385
    /organism="unknown"
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Unclassified.

Xu, Ju, Dillon, D.C., Mitcham, J.L., Harlocker, S.L. and Yuqiu, J. Prostate specific fusion protein compositions
Patent: US 6395278-A 67 28-MAY-2002;
Corixa Corporation; Seattle, WA
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Xu,J. and Dillon,D.C.
Compounds for immunotherapy of prostate
their use
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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Sequence 67 from patent US 6613872.
AR392284.1 GI:40116293

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    /organism="unknown"
    /mol_type="genomic DNA"

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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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Sequence 67 from patent US 6620922.
AR399919

    .385
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Xa,ds,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
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Sequence 67 from patent US 6759515.
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/mol_type="genomic DNA"
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                                  CTGGGCAGTCTTGCACATGAGATGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of pr
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Best Local Similarity 100.0%; Pred. No. 3.8e-117;
Matches 385; Conservative 0; Mismatches 0;
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Corixa Corporation; Seattle, WA;

    .385
    /organism="unknown"
    /mol_type="genomic DNA"

                                                                                                                                      CATAGTTTCTGTGCTAGTGGACCGT 385
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Sequence 67 from patent
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PAT 15-DEC-2004

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Unclassified.

1 (Dases 1 to 385)

Xu, J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Kalos,M.D., Fanger,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of prostate
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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/organism="unknown"
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Sequence 67 from patent US 6E
AR605372 GI:56657036
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Xalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
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                                                                                                                          Length 385;
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   06-JUL-2004;
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AR588552
AR58852.1 GI:56635449
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Patent: US 6759515-A 67 06-JU
Corixa Corporation; Seattle,
Location/Qualifiers
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Matches 385; Conservative
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1 (bases 1 to 385)

Xu,J. and Dillon,D.C.
Compounds for immunodiagnosis of prostate cancer and methods for
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Corixa Corporation; Seattle, WA
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate cancer

Patent: US 6894146-A 67 17-MAY-2005;
Corixa Corporation; Seattle, WA

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGENCOURT 6740305 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:58027375', mRNA Sequence.
                                                                                                                                    1,
                                                                                                                                                                                             248
                                                                                                                                                                                                                                                       308
                                                                                                                                                                                                                                                                                    190
                                                                                                                                                                                                                                                                                                                                                                           428
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbe-remail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM2037 row; j column: 18
High quality sequence stop: 751.
                                                                                                                                                                                                                                            CCACATCTCATGTGCAAGATTGCCCAGCAGAACAGGTCCAAGAGTTCCTGTTTTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                            TTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTGCCTCTCCCAG
                                                                                                                                                                TCCACTTGCCCTTGTGAGACACTTTGTCCCAGCACTTTAGGAATGCTGAGGTCGGACCAG
                                                                                                                                                                                            rcracrracccrrargagacacrrrarcccagcacrrraggaargcraaggcaa
                                                                                                                                                                                                                         CCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTCCCCTTTTAAAA
                                                                                                                                                                                                                                                                                      AAGGGGACTTGCTTAA-AAAAGAAGTCTAGCCACGATTGTGTAGAGCAGCTGTGCTGTGC
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1 (bases 1 to 986)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                    Gaps
                                                                                                                                    1;
                                                                                                      DB 9; Length 556;
                                                                                                                                  Indels
                                                                                                     Score 312.8; DB 9;
Pred. No. 4.2e-83;
0; Mismatches 27;
/db_xref="taxon:9606"
/clone="TESTI203332"
/tissue_type="testis"
/clone_Tib="TESTI2"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ068886.1 GI:19897932
                                                                                                     ttch 81.2%;
:al Similarity 92.4%;
340; Conservative
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Homo sapiens
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BQ068886/c
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KEYWORDS
SOURCE
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/tissue type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/dab_host="DH10B (phage-resistant)"
/done lib="WIH MGC_47"
/note="Organ: brianin; Vector: pOTB7; Site 1: Xho1; Site_2: EcoR1; cDNA made by oligo-dT priming. DIrectionally cloned into EcoR1/Kho1 sites using the following 5' adaptor: GGCACGA(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 TIGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTGCCTCTCCCAG
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCACATCTCATGTGCCAAGATTGCCCAGCAGCATCAGGTCTGAGAGTTCCCCTTTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 AAAGGGGACTTGCTTAAAAAAGAAGTCTAGCCACGATTGTGTAGAGCAGCTGTGCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 AAAGGGGACTTGCTCAAAAAAAAGAAGCCTGGCCATGTTTGTGTAAAAGAAGCAATGCTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 TGGAGATTCACTTTTGAGAGATCTCCTCTGAGACCTGATCTTTAGAGGCTGGGCAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                              Length 986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 RM10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
                                                                                                                                                                                                                                                                                                                                                                                              Score 231.8; DB 3;
Pred. No. 1.6e-58;
0; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD251924
AGENCOURT 14204354 NIH MGC_180 Ho
IMAGE:30383087 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD251924.1 GI:31012390
                                                                                                                                                                                                                                                                                                                                                                                                    60.2%;
88.0%;
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1 (bases 1 to 861)
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Gaps

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Length 491;

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Adminidae; Homo.

Is (bases 1 to 5483)

Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shemmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Altschul,S.F., Zeoberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Diatchenko,L., Marusina,K., Farmer,A.A., Whin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Mullak,J.B., Bosak,S.A., McEwan,P.J.,
Morley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzhy,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,T.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Mammalian Gene Collection Program Team
Human, A. M. A. Schein,J.E., Jones,S.J. and Marra,M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC063888 11near HTC 09-DEC-2005 Homo sapiens prostate-specific P704P mRNA, mRNA (cDNA clone IMAGE:30389199), with apparent retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   413 CCTAGCCTGGCCACACATGCTTACAGGGCACTCTTAGATGCCCACACTATAGCTGCCGTG 472
                                                                                                                                                                                                                                                                                                                                                                                                                      353 CACATGAGATGGGCTGGTCTGATGGCAGCACTCCTTANTCTGCTTGCCTCTCCCATGGC 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 CCCAGCCTGGCCACCTGCTTACAGGGCACTCTCAGATGCCCATACCATAGTTTCTGTG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                (http://www.evrogen.com) using their standard procedure.
See http://shark.ucsf.edu/~stas/report_MCF7.pdf for
details."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (08-DEC-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                        254 CACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTGCCTCTCCCAGGGC
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
cancer cell line by Evrogen JSC
                                                                                                                                                                                                           Score 111.8; DB 9; Length
Pred. No. 2.7e-22;
0; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BC063888.1 GI:39645658
                                                                                                                                                                                                              29.0%;
90.2%;
   MCF7 breast
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                                                                                                                                                                                                           Query Match
Best Local Similarity 90.23
Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 CTAGTGGACCGT 385
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TITLE
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REFERENCE
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BC063888
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COMMENT
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                                                                                              1..861
/organism="Momo sapiens"
/mol_type="mRNA"
/mb_xref="mRNA"
/db_xref="mRNA"
/db_host="MHAGE:30383087"
/lab_host="WHH MGC:3080087"
/lab_host="WHH MGC:3080087"
/clone lib="WHH MGC:180"
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/clone lib="WHH MGC:180"
/clone lib="WHH MGC:180"
/clone lib="multiple"
/
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MCF7RNAL2BP21TR Human MCF7 breast cancer cell line near full length normalized library (MCF7_EST) Homo sapiens cDNA clone
MCF7_RNA_L_28_P21, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hominidae; Homo.

1 (bases 1 to 491).

Volik, S. V., Raphael, B. J., Huang, G. -Q., Murnane, J., Brebner, J. H.,

Volik, S. V., Raphael, B. J., Huang, G. -Q., Murnane, J., Brebner, J. H.,

Shagin, D. A., Shagina, I. A., Magrane, G., Gray, J. W., Jan, F. -C., de

Jong, P., Pevzner, P. and Collins, C.

Decoding the genomic architecture and high throughput detection of
fusion transcripts in breast cancer cell lines: implications for a
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/clone_lib="Human MCF7 breast cancer cell line near full
length normalibrary (MCF7 EST)"
/note="Vector: pAL17; This library was constructed from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               272 TCTGATCTCAGCACTCCTTAGTCTGCTTGCCTCTCCCAGGGCCCCAGGCCTGGCCACCCT
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Pred. No. 2e-22;
0; Mismatches 1; Indels 0;
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Unpublished (2005)
Conteact: Volik SV
Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tex: 415 502 5665
Email: svolik@cc.ucsf.edu
Seg primer: SP6 5'-ATTTAGGTGACACTATAGAATAC-3'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="MCF7_RNA_L_28_P21"
/sex="female"
       column: 24
                                    High quality sequence stop: 701 Location/Qualifiers
   Plate: NDAM446 row: f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DN920910.1 GI:77951595
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99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 99.1
Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .. .491
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ORGANISM
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AUTHORS
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DN920910
                                                                        FEATURES
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Gaps

307

FEATURES

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Email: fll-cdna@mifty.com
NEDO human cDNA project (New Energy and Industrial Technology
Developmental Organization, Japan); cDNA library construction:
Helix Research Institute (HRI); 5'-end one pass sequencing: HRI,
Research Association for Biotechnology (RAB) and Biotechnology
Center, National Institute of Technology and Evaluation; 3'-end one
pass sequencing: RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                f. mura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T.,
Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H.,
Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N.,
Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M.,
Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A.,
Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.
Diversification of Transcriptional Modulation: Large-scale
Identification and Characterization of Putative Alternative
                                                                                                                 /tissue type="testis"
/clone_lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites SfilA + SfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           soss grerracaeraradarda de regrerea ecrea ecerce e de consecue e sos en esta en esta en esta en esta en esta e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 GICTIGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTGCCTCCC
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Helix Resear(h Institute
2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan
Tel: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                    Length 6098;
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                                                                                 26.4%; Score 101.8; DB 6 93.8%; Pred. No. 5.4e-19;
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/mol_type="mRNA"
/db_xref="RZD90:DKF2p686J0529Q"
/db_xref="taxon:9606"
/clone="DKF2p686J0529"
                                                                                                                                                                                                                                            /note="putative transcript"
                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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/db_xref="taxon:9606"
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                                                                                                                                                                                                               /dev stage="adult"
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DA554900.1 GI:80884861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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1 (bases 1 to 553)
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                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                   Similarity
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ses 106;
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DA554900
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Homo sapiens mRNA; cDNA DKFZp686J0529 (from clone DKFZp686J0529).
BX649118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3936 TCCCAGCACTCCTTAGTCTGCTTTGCCTCTCCCAGGCCCCCAGCCTGGCCACCTGCTTA 3995
                               info@bcgsc.bc.ca
Martin Hirst, Thomas Zeng, Ryan Morin, Michelle Moksa, Johnson
Pang, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
Peng, Diana Mah, Jing Wang, Kieth Fichter, Eric Chuah, Allen
Delaney, Rob Kirkpatrick, Agnes Baross, Sarah Barber, Mabel
Brown-John, Steve S. Chand, William Chow, Ryan Babakaiff, Dave
Wong, Corey Matsuo, Jaclyn Beland, Susan Gibson, Luis delRio, Ruth
Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
Kim MacDonald, Mike R. Mayo, Josh Moran, Diana Palmquist, JR
Santos, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang,
Jacquie Schein, Asim Siddiqui, Steven Jones, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be found
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 TCTCAGCACTCCTTAGTCTGCCTTCCCCAGGCCCCCAGCCTGGCCACCTGCTTA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686J0529
Further information about the clone and the sequencing project is
available at http://mips.gsf.de/projects/cdna/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                            through the I.M.A.G.E. Consortium/Linn at: http://image.llnl.gov
Series: IRAK Plate: 141 Row: o Column: 10
This clone has the following problem: retained intron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-JAM-2005) MIPS, Ingolstaedter Landstr.1, D-85764
Neuherberg, GERMANY
Clone From S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZD686J0529) is available at the RZPD Deutsches
Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZPD for ordering:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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1 (bases 1 to 6098)
Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and Wiemann,S.
The German cDNA Consortium
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3996 CAGGGCACTCTCAGATGCCCATACCATAGTTTCTGTGCTAGTGGACCGT 4044
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Pred. No. 1.1e-20;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/mol_type="mRNA"
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/clone="type="Testis"
/tissue_type="Testis"
/lab host="blio"
/note="vector: pCMV-SPORT6.1"
      Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/organism="Homo sapiens"
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Best Local Similarity 99.1%;
Matches 108; Conservative
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Homo sapiens
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

TITLE JOURNAL

COMMENT

CONSRTM

AUTHORS REFERENCE

source

FEATURES

RESULT 6 HSM809270/c

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                                                                261 ATGGCCAGGCTTCTTTTTGAGCAAGTCCCCTTTTTGAAGAGGGGAACTCTGGGAACTGA 320
                                                                                                                             TCTTTAGAGGCTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTT 290
                                                                                                                                                                 TCTCT----GCTGGGCAGTCTTGAAAATGAGATGGGCTGATCTGAACTTAGCATTCCTA 376
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Is I (bases 1 to 873)

Is Nath-MCC http://mgc.nci.nih.gov/.

In WaC http://mgc.nci.nih.gov/.

In Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 RanloAO' Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

CDNA Library Preparation: Invitrogen Corp

CONA Library Preparation: Invitrogen Corp

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM446 row: e column: 23

High quality sequence stop: 540.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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         171 GTAGAGCAGCTGTGCTGTGCAGATTCACTTTTGAGAGAGTTCTCCTCTGAGACCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 TCTGATCTCAGCACTCCTTAGTCTGCCTTGCCTCTCCCAGGGCCCCAGCCTGGCCACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD251853 873 bp mRNA linear EST
AGENCOURT 14206078 NIH MGC_180 Homo sapiens cDNA clone
IMAGE:30383062 5′, mRNĀ sequence.
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Pred. No. 1.1e-16;
0; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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CD251853.1 GI:31012319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 24.3%;
il Similarity 93.9%;
108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
Homo sapiens
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Best Local S:
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TITLE
JOURNAL
COMMENT
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KEYWORDS
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/lab_host="BH10B (phage-resistant)"
/lab_host="BH10B (phage-resistant)"
/clone_lib="NHH_MGG_47"
/note="Organ: brain; Vector: pOTB7; Site 1: Xho1; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/KhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california. Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                            986 bp mRNA linear EST 02-APR-2002
AGENCOURT_6740305 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802737
S, mRNA sequence.
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                                                                                                                                                                                                                                           240 GCTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTT 299
                                                                                                                                                                 141 GGAGTGCTGATATCAGACCAGCCCCATCTCATGTGCAGGACTGCCCAGCAGAGATCAGGT 200
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image-llnl.gov
Plate: LLCM2037 row; j column: 18
High quality sequence stop: 751.
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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   Length 553;
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                                                                Indels
                                                                12;
      Score 100.8; DB 9;
                                   Pred. No. 5.8e-19;
0; Mismatches 12
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Pred. No. 3.8e-17;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5802737"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQ068886.1 GI:19897932
26.2%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae; Homo.
1 (bases 1 to 986)
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Best Local Similarity 65.1:
Matches 157; Conservative
                                                                Conservative
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                                   Similarity
                                Best Local Simi
Matches 108;
      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
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BQ068886
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Hominidae, Homo.

I (bases 1 to 6098)

S Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
The German CDNA Consortium
Direct Submission
Submitted (120-JAN-2005) MIPS, Ingolstaedter Landstr.l, D-85764
Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s. wiemann@dkfz-heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp6860529) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please conteat RZPD for ordering:
thtp://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp686J0529
Further information about the clone and the sequencing project is available at http://www.rzpd.de/cmips.gef.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGU55887 628 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-055G12.F, genomic survey sequence.
AG065887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="testis"
/clone lib="686 (synonym: hlcc3). Vector pSport1_Sfi; host
DH10B; sites Sfi1A + Sfi1B"
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 CACTCCTTAGTCTGCTTGCCTCTCCCAGGGCCCCAGGCCTGGCCACACCTGCTTACAGGGC
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11.8%; Score 83.8; DB 6; Similarity 88.3%; Pred. No. 1.5e-13; 91; Conservative 0; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="R2PD:DKF2p686J0529Q"
/db xref="taxon:9606"
/clone="DKF2p686J0529"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="putative transcript"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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AG065887/c
LOCUS
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BX649118.1 GI:34368290
HTC.
                                                                                                                                                                                                                                                                                                                                                                                                                    Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission

Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-50-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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                                                GSS 03-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AG106788 660 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-111G14.R, genomic survey sequence.
                                                                                                                                                                                        Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /eex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-111G14.R"
                                                                                                                                                                                                                                                                                                       Fuliyama, A., Hattori, M., Toyoda, A., 'Totoki, Y., Watanabe, H. and Sakaki, Y. BAC end sequences of Library PTB
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                                                                                                                                                                    Pan troglodytes (chimpanzee)
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Hominidae; Homo.
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Best Local Similarity
Matches 90; Conserv
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CR748036/c
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Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB.
Unpublished

2 (bases 1 to 704)

S Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission

L. Submitted (02-A04-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN) Genomic Sciences Center (GSC);
1-7-2 Suehiro-chou, Tauruni, Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-85-503-9111, Fax:81-85-503-9170

Clones are derived from the chimpanzee BAC library PTB This BAC end
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Pan troglodytes DNA, clone: PTB-094P10.R, genomic survey sequence.
AG094252
was generated during the R&D process and may have higher chance of
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini;
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                                                                                                                                                                  1. 628
/organism="Pan troglodytes"
/organism="Pan troglodytes"
/organism="Pan troglodytes"
/db_xref="taxon:9599"
/clone="PTB-055G12.F"
/sex="manle"
/cell type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                    Length 628;
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                                                                                                                                                                                                                                                                                                                                                                Query Match 20.1%; Score 77.4; DB 14;
Best Local Similarity 74.2%; Pred. No. 7.2e-12;
Matches 115; Conservative 0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               351 ATGCCCATACCATAGTTTCTGTGCTAGTGGACCGT 385
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Pan troglodytes
                                                                                           Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
                                                       Sequencing: -21M13
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R.Site 1 : SacI
R.Site 2 : SacI.
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                 clone tracking errors.
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CR748036 CR748036 B61 bp mRNA linear EST 21-DEC-2004 CR748036 Homo sapiens library (Ebert L) Homo sapiens cDNA clone IMAGP998D104117; IMAGE:1623129 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          215 GCAGGTCAGTCTTGCACATCAGATGGGGCTGGCCTGAACTGAGTACCCCCTATCCTCCTG 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Ebert, L., Heil, O., Hennig, S., Korn, B., Newbert, P., Partsch, E. Peters, M., Radelof, U. and Schneider, D.
I.M. A.G.E. CDNA Clone Collection
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Inge Arlart

READ Deutsches Ressourcenzentrum fuer Genomforschung GmbH

Heubnerweg 6, D-14059 Berlin, Germany

Email: www.rzpd.de

REZPD; IMAGP998D104117.

RZPDIIB; I.M.A.G.E. CDNA Clone Collection;

Contact: Inge Arlart
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Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
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0
                                                                                                                                                                                                                                                              Score 74.4; DB 14; Length 704;
Pred. No. 6e-11;
0; Mismatches 26; Indels 0
                                                                                                                                         /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 861;
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19.3%; Score 74.2; DB 8; Length 8
Best Local Similarity 72.9%; Pred. No. 7.3e-11;
Matches 113; Conservative 0; Mismatches 33; Indels
organism="Pan troglodytes"

    .861
    /organism="Homo sapiens"

                     /mol type="genomic DNA"
/db xref="taxon:9598"
/clone="PTB-094P10.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CR748036
CR748036.1 GI:51661862
                                                                                                                                                                                                                                                        ch 19.3%;
1 Similarity 77.6%;
90; Conservative (
                                                                                                                    /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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Hominidae; Homo.
1 (bases 1 to 527)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mahairas,G.G., Wallace,J.C., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
                                                                                                                                                                                                                                   AQ784117 527 bp DNA linear GSS 03-AUG-1999
HS_3034_B1_A11_T7C CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3034 Col=21 Row=B, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   253 GCGGGGCAGTCTTGCCCCTGAGACAGGGCCAGTCTGACCTGAGCATCCTTCAGTCTGCTC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
BAC end web Server: http://www.htsc.washington.edu
Seq primer: T7
Class: BAC ends
Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="male"
/clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 10449764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 GCCCTCCTGTGGCCCCAGCCTGCCTGCTTGCAGTGCAGCTTCACA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
19.1%; Score 73.6; DB 11; Length 527;
Best Local Similarity 78.6%; Pred. No. 9.8e-11;
Matches 88; Conservative 0; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db xref="taxon:9606"
/clone="plate=3034 Col=21 Row=B"
                                                                        355 ----CCATACCATAGTTTCTGTGCTAGTGGACCGT 385
                                                                                                Search completed: December 31, 2006, 19:30:49 Job time : 3091.06 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 527.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  AQ784117
AQ784117.1 GI:5691741
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                        RESULT 15
AQ784117
LOCUS
DEFINITION
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PUBMED
COMMENT
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AUTHORS
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FEMOLEGATION STATEMENT OF THE STATEMENT OF S
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Sequence 11258, A
Sequence 701, App
                                                                                                                                                                                      December 31, 2006, 12:22:01; Search time 613.045 Seconds (without alignments) 7716.790 Million cell updates/sec
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-822-827-67
US-09-115-453-67
US-09-232-880-67
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US-10-688-838-67
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US-09-895-814-67
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US-10-010-940-67
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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No.
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C23
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100.0%; Score 385; DB 3; L
Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
Sequence 67, Application US/09759143
Patent No. US20020022248A1
                                                                                                               Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
                                                         Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
                                                                                                                                                                                                                                     Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                         Skeiky, Yasir A.W.
Hepler, William
                                                                                                                                                                                                Fanger, Gary R.
Retter, Marc W.
                                                                                                                                                                                                                                                                                                                                             Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                        Samue
                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 67
LENGTH: 385
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
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1 ACTACACACACTCCACTTGCCCTTGTGAGACACTTTGTCCCAGCACTTTAGGAATGCTGA 60

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Gaps

180 180 240

240

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Sequence 67, Application US/09030606

Patent No. US20020081580A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
ITILE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHODS F
ITILE OF INVENTION: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seatile
STATE: WA
                                                                                                                                                                                                                                                                 301 CCTCTCCCAGGGCCCCAGGCTGGCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
                                                                                                                                                                                                                                                                                                                                       301 CCTCTCCCAGGGCCCCAGCCTGGCCACACCTGCTTACAGGGCACTCTCAGATGCCCATAC 360
                                   61 GGTGGGACCAGCCACATCTCATGTGCAAGATTGCCAGCAGCACAGCACTGAGGTCTGAGAGTTC
                                                                                                                                                                                         181 TGGCTGTGCGAGATTCACTTTTGAGAGAGTTCTCCTCTGAGAGACCTGATCTTTAGAGG
                                                                                                                                                                                                                                           CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG
                                                                                                             TGTGCTGTGCTGGAGATTCACTTTTGAGAGTTCTCCTCTGAGACCTGATCTTTAGAGG
                                                                                         CCCTTTTAAAAAAGGGGACTTGCTTAAAAAAGAAGTCTAGCCACGATTGTGTAGAGCAGC
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Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/030,606
FILING DATE: 25-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   385
                                                                                                                                                                                                                                                                                                                                                                                                361 CATAGTTTCTGTGCTAGTGGACCGT 385
                                                                                                                                                                                                                                                                                                                                                                                                                       CATAGTTTCTGTGCTAGTGGACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 base pairs nucleic acid
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US-09-030-606-67
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CCCTTTAAAAAAGGGGGCTTCTTAAAAAAGAAGTCTAGCCACGATTGTGTAGAGCAGC
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                                                                                                                                                                                                                              GGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NHBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
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Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0;
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Patent No. US20020051977A1
GENERAL INFORMATION:
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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McNeill, Patricia D.
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Henderson, Robert A.
Kalos, Michael D.
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Skeiky, Yasir A.W.
Hepler, William
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Vedvick, Thomas S.
Carter, Darrick
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Retter, Marc W.
Stolk, John A.
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ORGANISM: Homo sapien
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SEQ ID NO 67
LENGTH: 385
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US-09-780-669-67
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APPLICANT:
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Patent No. U520020090372A1
Patent No. U520020090372A1
Patent No. U520020090372A1
APPLICANT: W. Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND TITLE OF INVENTION: COMPOUNDS FOR THEIR USE FILE REPERENCE: 210121.427C4
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ 1D NOS: 228
SOFTWARE: FARSEQ for Windows Version 3.0
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Publication No. US20020182596A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Nu. Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
FILE REFERENCE: 210121.42866
CURRENT APPLICATION NUMBER: US/09/232,880
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Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0;
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CORGANISM: Homo sapien
US-09-115-453-67
                                                           361 CATAGTT
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US-09-115-453-67
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US-09-232-880-67
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                         ACTACACACACTCCACTTGCCCTTGTGAGACACTTTGTGCCGACCACTTTAGGAATGCTGA
                                                                               GGTCGGACCAGCCACATCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC
                                                                                                   GGTCGGACCACCACTCTCATGTGCAAGATTGCCCAGCAGACATCAGGTCTGAGAGTTC
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   ACTACACACACTCCACTTGCCCTTGTGAGACACTTTTGTCCCAGCACTTTAGGAATGCTGA
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Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT APPLICATION NUMBER: US/09/822,827
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 100.(
Matches 385; Conservative
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; ORGANISM: Homo sapien
US-09-822-827-67
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APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
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                                                                                                                                                                                                                                                      100.0%; Score 385; DB 3; Length 385; 100.0%; Pred. No. 2.2e-126; Live 0; Mismatches 0; Indels
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
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Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
McWelll, Patricia D.
Houghton, Raymond L.
Vinale de Bassols, Carlota
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                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 385; Conservative
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                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-793-67
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 21012.1.5342.
CURRENT APPLICATION NUMBER: US/09/895,793
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100.0%; Pred. No. 2.2e-126;
ive 0; Mismatches 0;
                           NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
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Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020192763A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Rater, Marc W.
APPLICANT: Stolk, John A.
         CURRENT FILING DATE: 1999-01-15
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Vedvick, Thomas S.
Carter, Darrick
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Best Local Similarity 100.
Matches 385; Conservative
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CORGANISM: Homo sapien
US-09-232-880-67
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APPLICANT: Reter, Gary
APPLICANT: Reter, Mark
APPLICANT: Sol, John
APPLICANT: Sol, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 2.10.12.4.27D3
CURRENT APPLICATION NUMBER: US/10/010,940
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Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0;
                CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
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Jiang Yuqui
Reed, Steven G.
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
FILE REFERENCE: 210121.427C27
                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
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CORGANISM: Homo sapien
US-10-010-940-67
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
APPLICE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                   Length 385;
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                              100.0%; Score 385; DB 3; L ilarity 100.0%; Pred. No. 2.2e-126; Conservative 0; Mismatches 0;
                    NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 67
LENGTH: 385
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020183251A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
2001-06-29
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Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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Hepler, William T.
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                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-895-814-67
CURRENT FILING DATE:
                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 385; Conserv
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US-10-012-896-67
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                                                   ; DB 7; Length 385; 2.2e-126;
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; Sequence 67, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jianghun
; APPLICANT: Stolk, John A.
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427029
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSEQ for Windows Version 3.0
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100.0%; Pred. No. 2.2e-126;
ive 0; Mismatches 0;
                                                                                          0; Mismatches
                                                     100.0%; Score 385;
100.0%; Pred. No. 2
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Best Local Similarity 100.
Matches 385; Conservative
                                                     Query Match
Best Local Similarity 100.
Matches 385; Conservative
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CORGANISM: Homo sapiens
US-10-294-025-67
                US-10-144-678A-67
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                                                         Gaps
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APPLICANT: Denoy, Ta.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OP PROSTATE CANCER
FILE REFERENCE: 210121.427C28
CURRENT PELLIGA DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SEQ ID NO 67
SEQ ID NO 67
LENGTH: 385
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                  DB 6; Length 385;
                                                       0; Indels
                  Score 385; DB 6; L
Pred. No. 2.2e-126;
100.0%; Scc. No. 4.100.0%; Pred. No. 4.100.0%; Pred. No. 4.100.0%; O. Mismatches
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals y de Bassols, Carlota
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Hitcham, Jennifer L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Ralos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
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Watanabe, Yoshihiro
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Skeiky, Yasir A. W.
Hepler, William T.
                                       Best Local Similarity 100.
Matches 385, Conservative
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ORGANISM: Homo sapiens
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US-10-144-678A-67
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APPLICANT:
                  Query Match
Best Local
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US-11-234-786-67
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                                                CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG
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                                                                                                                                                                                                                                                                                           Sequence 67, Application US/10688838

Publication No. US20040141989A1

GENERAL INFORMATION:

APPLICANT: W. JUANGOUND

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE

TITLE OF INVENTION: COMPOUNDS FOR THEIR USE

FILE REFERENCE: 210121.427D4

CURRENT APPLICATION NUMBER: US/10/688,838

CURRENT FILING DATE: 2003-10-17

NUMBER OF SEQ ID NOS: 228

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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Best Local Similarity 100.0%; Pred. No. 2.2e-126;
Matches 385; Conservative 0; Mismatches 0;
                                                                                                                                                                                 CATAGTTTCTGTGCTAGTGGACCGT 385
                                                                                                                                                                                                      CATAGITICIGIGCIAGIGGACCGI 385
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US-11-234-786-67
Sequence 67, Application US/11234786
; Publication No. US20060024301A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                 RESULT 13
US-10-688-838-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Skeik, Yaair A.

TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
TITLE OF INVENTION: PLOYPEPTIDES THEREOF
FILE REFERENCE: 21012-142731
CURRENT PILING DATE: 2005-09-23
CURRENT FILING DATE: 2006-09-03
FRIOR PILING DATE: 2000-05-09
FRIOR APPLICATION NUMBER: US 09/568,857
FRIOR APPLICATION NUMBER: US 09/536,857
FRIOR APPLICATION NUMBER: US 09/433,672
FRIOR APPLICATION NUMBER: US 09/433,672
FRIOR PILING DATE: 2000-01-14
FRIOR FILING DATE: 1999-11-12
FRIOR PILING DATE: 1999-11-13
FRIOR PILING DATE: 1999-07-13
FRIOR PILING DATE: 1999-07-15
FRIOR FILING DATE: 1999-01-15
FRIOR FILING DATE: 1999-02-25
FRIOR FILING DATE: 1999-02-25
FRIOR FILING DATE: 1998-02-25
FREMAINING PRICE PRESOF FOR WINDOWS 701
FRIOR FILING DATE: 1998-03-25
FREMAINING PRICE PRESOF FOR WINDOWS 701
FROM FILING DATE: 1998-03-25
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100.0%; Pred. No. 2.2e-126;
ive 0; Mismatches 0;
                                                                                               Harlocker, Susan L.
Jiang, Yugiu
Reed, Steven G.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
(u, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 385; Conservative
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us-09-232-880-67.rnpbm

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241 CTGGGCAGTCTTGCACATGAGATGGGGCTGGTCTGATCTCAGCACTCCTTAGTCTGCTTG 300
                                                      2282 ACCACACACTCCACTTGCCCTTGTGAGACACTTTGTCCCAGCACTTTAGGAATGCTGA
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                                                                                                                                                                                                                         ; Sequence 1036, Application US/10294025
; Publication No. US20030185830A1
; CENERAL INFORMATION:
; APPLICANT: Xu Jungchun A.
; APPLICANT: Xtolk, John A.
; APPLICANT: Stolk, John A.
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 20022-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOOTWARE: FESTSEQ for Windows Version 3.0
; LENGTH: 3710
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99.2%; Score 381.8; DB 7; Length 3710;
Best Local Similarity 99.5%; Pred. No. 8.4e-125;
Matches 383; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2642 CATAGTTTCTGTGCTAGTGGACCGT 2666
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                                                                                                          CATAGITICIGIGCTAGIGGACCGI 385
                                                                                                                              ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-294-025-1036
                                                                                                                                                                                                   RESULT 15
US-10-294-025-1036
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Search completed: December 31, 2006, 13:56:03 Job time : 615.045 secs

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| FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
| FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
| FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
| FEMC_Celerra_SIDS3/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
| FEMC_Celerra_SIDS3/ptodata/2/pubpna/DSO8_NEW_PUB.seq:*
| FEMC_Celerra_SIDS3/ptodata/2/pubpna/US10_NEW_PUB.seq:*
| FEMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                                                                                                                                                                                  December 31, 2006, 12:26:03; Search time 557.33 Seconds (without alignments) 6266.684 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3050214 segs, 1077301958 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published_Applications_NA_New:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                               US-09-232-880-107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
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                                                                                                                                                                                                                                                                                                                               Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

		ď			SOUTHERNIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ΙD	Description
1	1621	100.0	1621	- '	US-11-344-932-107	Seguence 107, App
2	1621	100.0	1621	10	US-11-349-541-107	Semience 107. App
l W	1574.2	97.1	2005	ω	US-11-266-748A-23190	Sequence 23190, A
4	1574.2	97.1	2005	10	US-11-343-797-104	Sequence 104, App
S	1571	96.9	2041	æ	US-11-266-748A-22797	Sequence 22797, A
9	1524.8	94.1	2068	8	US-11-266-748A-23899	Sequence 23899, A
7	1240.6	76.5	2373	æ	US-11-266-748A-57286	Sequence 57286, A
ر 8	882.2	54.4	971	8	US-11-266-748A-215905	Sequence 215905,
6	882.2	54.4	971	œ	US-11-266-748A-237887	Sequence 237887,
10	783	48.3	958	æ	US-11-266-748A-46436	Sequence 46436, A
11	734.6	45.3	924	8	US-11-266-748A-84584	Sequence 84584, A
12	734.6	45.3	924	ω	US-11-266-748A-111891	Sequence 111891,
c 13	734.6	45.3		ω	US-11-266-748A-137395	Sequence 137395,
14	515	31.8	537	7	US-11-344-932-74	Sequence 74, Appl
15	515	31.8		10	US-11-349-541-74	Sequence 74, Appl
16	514	31.7	554	ω	US-11-266-748A-349470	Sequence 349470,
c 17	514	31.7		œ	US-11-266-748A-432849	Sequence 432849,
18	513.6	31.7		œ	US-11-266-748A-371009	Sequence 371009,
c 19	513.6	31.7	932	œ	US-11-266-748A-454388	Sequence 454388,
c 20	447.8	27.6	625	10	US-11-190-172-4076	Sequence 4076, Ap
21	426.8	26.3	430	œ	US-11-301-554-1504	Sequence 1504, Ap
22	424	26.2	597	7	US-11-371-354-4921	Sequence 4921, Ap

Sequence 59156, A	Sequence 3, Appli	Sequence 3, Appli	Sequence 33, Appl	Sequence 33, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 252, App	Sequence 242, App	Sequence 6, Appli	Sequence 380888,	Sequence 464267,	Sequence 224722,	Seguence 246615,	Sequence 398998,	Seguence 470044,	Sequence 84585, A	Sequence 111892,	Sequence 137396,	Sequence 16830, A	Sequence 2253, Ap	Sequence 10189, A	Seguence 11125, A	
US-11-371-354-59156	US-11-344-932-3	US-11-349-541-3	US-11-344-932-33	US-11-349-541-33	US-11-344-932-2	US-11-349-541-2	US-11-344-932-252	US-11-344-932-242	US-10-527-552-6	US-11-266-748A-380888	US-11-266-748A-464267	US-11-266-748A-224722	US-11-266-748A-246615	US-11-266-748A-398998	US-11-266-748A-470044	US-11-266-748A-84585	US-11-266-748A-111892	US-11-266-748A-137396	US-11-292-078-16830	US-11-292-078-2253	US-11-292-078-10189	US-11-292-078-11125	
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424	406.6	406.6	403.2	403.2	400.2	400.2	275.4	272.4	234.8	189.4	189.4	121.4	121.4	121.4	121.4	104	104	104	81	79.4	76.8	75.6	
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ALIGNMENTS

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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C32
CURRENT APPLICATION NUMBER: US/11/344,932
CURRENT FILING DATE: 2006-02-01
PRIOR APPLICATION NUMBER: 10/144,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carlota
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PRIOR APPLICATION NUMBER: 10/012,896
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 09/895,814
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
PRIOR FILING DATE: 2001-05-09
                    Sequence 107, Application US/11344932
Publication No. US20060269532A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals y de Bassols, C?
Foy, Teresa M.
                                                                                  APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jang, Yuqiu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watanabe, Yoshihiro
Meagher, Madeleine Joy
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Hepler, William T.
                                                                                                                                                                                                                                          Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
                                                                                                                                                                                                                                                                                                                                                                                 Samuel X.
                                                                                                                                                                                                                                                                                                                                                                                                      Wang, Aijun
US-11-344-932-107
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US-11-349-541-107
Sequence 107, Application US/11349541
Sequence 107, Application WS/12081
Sequence 107, Application No. US20060223129A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND
TITLE OF INVENTION: METHODS FOR THEIR USE
TITLE OF 10121.428C7
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100.0%; Pred. No. 4e-304;
ive 0; Mismatches 0
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PRIOR APPLICATION NUMBER: 09/759,143
PRIOR FILING DATE: 2001-01-12
PRIOR PLING DATE: 2001-01-09
PRIOR PLING DATE: 2000-11-09
PRIOR PLING DATE: 2000-11-09
PRIOR PLING DATE: 2000-10-10
PRIOR PLING DATE: 2000-10-10
PRIOR PELICATION NUMBER: 09/679,426
PRIOR PLING DATE: 2000-10-02
PRIOR PELING DATE: 2000-00-05
PRIOR FILING DATE: 2000-00-06
PRIOR FILING DATE: 2000-00-06
NUMBER OF SEQ ID NOS: 1033
NUMBER OF SEQ ID NOS: 1033
SEQ ID NO 107
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; ORGANISM: Homo sapiens
US-11-344-932-107
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Matches 1621; Conser
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Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Partick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
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CURRENT APPLICATION NUMBER: US/11/349,541
CURRENT FILING DATE: 2006-02-06
PRIOR PELLING DATE: 1080-07-14
PRIOR FILING DATE: 1980-07-14
PRIOR FILING DATE: 1998-07-15
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: US 09/020,747
PRIOR APPLICATION NUMBER: US 08/020,747
PRIOR APPLICATION NUMBER: US 08/904,809
PRIOR APPLICATION NUMBER: US 08/904,809
PRIOR APPLICATION NUMBER: US 08/906,596
PRIOR FILING DATE: 1997-02-25
NUMBER OF SEQ ID NOS: 228
SEQTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                              Query Match
100.0%;
Best Local Similarity 100.0%;
Matches 1621; Conservative 0
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99.8%; Pred. No. 4.7e-295;
ive 0; Mismatches 3; Indels
TITLE OF INVENTION: Methods of Using the Sammer File Reference: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105492.
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
                                                                                                                                                                                                                                                                                                                                                                                     Matches 1576; Conservative
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; ORGANISM: Homo Sapiens
US-11-266-748A-23190
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Publication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
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                                                           Prostate Cancer
            APPLICANT: Rubin, Mark A.
APPLICANT: Sreekumar, Arun
TITLE OF INVENTION: Expression Profile of Profile OF INVENTION: Expression Profile of Profile OF INVENTION: Expression Profile of Profile OF INVENTION: BY STATEMENT FILING DATE: 2006-01-31
PRIOR PILING DATE: 2002-08-01
PRIOR PLING DATE: 2001-08-02
PRIOR PILING DATE: 2001-08-02
PRIOR PILING DATE: 2001-08-03
PRIOR PILING DATE: 2001-11-15
NUMBER: OF SEQ ID NOS: 123
SEQ ID NO 104
LENGTHR: 2005
LENGTHR: 2005
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LENGTHR: 2005
APPLICANT: Chinnaiyan, Arul M.
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Matches 1576; Conservative
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; Sequence 23899, Application US/11266748A
; Publication No. US20060134663A1
; GENERAL INFORMATION:
; APPLICANT: Harkin, Paul
; APPLICANT: Obnston, Patrick
; APPLICANT: Mulligan, Karl
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.larity 99.7%; Pred. No. 2e-294;
Conservative 0; Mismatches 5; Indels 0
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-11-03
PRIOR FILING DATE: 2005-03-14
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Pred. No. 1.7e-285;
0; Mismatches 18;
                     Using the Same
TITLE OF INVENTION: Transcriptome Microarray 7
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (139189)
CURRENT PEDELICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-03-14
NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
NUMBER OF SEQ ID NOS: 483996
SEQ ID NO 23899
LENGTHARE: PATENTIN VERSION 3.3
SEQ ID NO 23899
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: LOCATION: (143)..(143)

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US-11-266-748A-23899
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Best Local Similarity 98.6%;
Matches 1559; Conservative
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Pred. No. 1.6e-230;
0; Mismatches 4; Indels 161;
            US-11-266-748A-57286

| Sequence 57286, Application US/11266748A
| Publication No. US20060134663A1
| GENERAL INFORMATION:
| APPLICANT: Harkin, Paul
| APPLICANT: Holmston, Patrick
| APPLICANT: Mulligam, Karl
| TITLE OF INVENTION: Methods of Using the Same
| TITLE OF INVENTION: Methods of Using the Same
| TITLE OF INVENTION: Methods of Using the Same
| FILE REFERENCE: 55815-0102 (339189)
| CURRENT APPLICATION NUMBER: US/11/266,748A
| CURRENT APPLICATION NUMBER: EP 04105492.2
| PRIOR FILING DATE: 2004-11-03
| PRIOR FILING DATE: 2004-11-03
| PRIOR APPLICATION NUMBER: EP 04105482.6
| PRIOR APPLICATION NUMBER: EP 04105482.6
| PRIOR APPLICATION NUMBER: EP 04105482.9
| PRIOR PILING DATE: 2004-11-03
| PRIOR PILING DATE: 2004-11-03
| PRIOR FILING DATE: 2005-03-14
| PRIOR PLING DATE: 2005-03-14
| PRIOR FILING DATE: 2005-03-14
| PRIOR PLING DATE: 2
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Best Local Similarity 89.6%;
Matches 1414; Conservative
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US-11-266-748A-57286
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APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR APPLICATION NUMBER: EP 04105482.6
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APPLICANT: Harkin, Paul
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Sequence 215905, Application US/11266748A

Publication No. US20660134663A1

GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Harkin, Paul
ITILE OF INVENTION: Transcriptome Microarray Technology and
ITILE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)

CURRENT APPLICATION NUMBER: US/11/266,748A

CURRENT APPLICATION NUMBER: EP 04105479.2

PRIOR PAPLICATION NUMBER: EP 04105479.2

PRIOR PAPLICATION NUMBER: EP 04105482.6

PRIOR PLING DATE: 2004-11-03

PRIOR PELING DATE: 2005-07-18

NUMBER OF SEC ID NOS: 483996

PROPERTY OF SEC ID NOS: 483996
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// LOCATION: (893)
// OTHER INFORMATION: n is a, c, g,
US-11-266-748A-215905
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SEQ ID NO 215905
LENGTH: 971
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Best Local Similarity 96.3%
Matches 893; Conservative
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OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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FEATURE:
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NAME/KEY: misc_feature
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Patrick
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 58815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2006-11-03
FRIOR FILING DATE: 2004-11-03
FRIOR PILING DATE: 2005-10-11-03
FRIOR APPLICATION NUMBER: US 60/662,276
FRIOR PILING DATE: 2005-11-03
FRIOR PILING DATE: 2005-07-18
FRIOR FILING DATE: 2005-07-18
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ORGANISM: Homo Sapiens
FEATURE:
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SEQ ID NO 46436
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 PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
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PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
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; DCATION: (948)...(949)
; OTHER INFORMATION: n is a, c, g, or
US-11-266-748A-237887
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NAME/KEY: misc_feature
LOCATION: (79) ...(79)
OTHER INFORMATION: n is a, c,
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NAME/KEY: misc_feature
LOCATION: (933) ...(933)
OTHER INFORMATION: n is a, c,
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NAME/KEY: misc feature
LOCATION: (936)..(937)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
FEATURE:
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ORGANISM: Homo Sapiens
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                                                                                                    Length 958
                                                                                                                                        Indels
                                                                                                                                          31;
                                                                                                  Score 783; DB 8; 1
Pred. No. 3.7e-142;
0; Mismatches 31;
                                         or
                    ; LOCATION: (709)
; OTHER INFORMATION: n is a, c, g,
US-11-266-748A-46436
                                                                                                Query Match
Best Local Similarity 95.8%;
Matches 858; Conservative
NAME/KEY: misc_feature
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APPLICANT: Harkin, Paul
APPLICANT: Johnston, Patrick
APPLICANT: Johnston, Rarl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
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Pred. No. 8.3e-133;
0; Mismatches 14;
                                                                                                 TITLE ROF INVENTION: MECHOGA OI USING THE SAME
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR PRILING DATE: 2005-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2005-101-03
PRIOR PILING DATE: 2005-07-18
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 84584
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LOCATION: (903)..(903)
1 O'TER INFORMATION: n is a, c,
US-11-266-748A-84584
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LOCATION: (773)..(773)
OTHER INFORMATION: n is
FEATURE:
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OTHER INFORMATION: n is
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ORGANISM: Homo Sapiens
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RESULT 11 US-11-266-748A-84584 ; Sequence 84584, Application US/11266748A

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45.3%; Score 734.6; DB 8;
Best Local Similarity 97.7%; Pred. No. 8.3e-133;
Matches 798; Conservative 0; Mismatches 14;
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OTHER INFORMATION: n is a,
FEATURE:
NAME/KEY: misc_feature
) COCATION: (873)... (873)
OTHER INFORMATION: n is a,
FEATURE:
NAME/KEY: misc_feature
) LOCATION: (873)... (873)
OTHER INFORMATION: n is a,
CATION: (903)... (903)
US-11-266-748A-111891
NAME/KEY: misc feature
LOCATION: (773)...(773)
OTHER INFORMATION: n is a
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NAME/KEY: misc feature
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                          300 TCTTTCAAAAGGGATCCTTTCATAGGAGAAACACACTGAGGAGATACTTGAAGAATTTGGA 359
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APPLICANT: HARTAI, PAUL
APPLICANT: Mulligan, Karl
APPLICANT: Mulligan, Karl
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PELING DATE: 2004-11-03
PRIOR PELING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR FILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-14
PRIOR PILING DATE: 2005-03-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
SEQ ID NO 111891
LENGTH: 924
TYPE: DNA
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APPLICANT: Harkin, Paul
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US-11-266-748A-111891
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805 ACGAAGCCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTG 746
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Publication No. US20060269532A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
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Houghton, Raymond L.
Vinals y de Bassols,
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Hepler, William T.
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Vedvick, Thomas
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Retter, Marc W.
Stolk, John A.
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APPLICANT: HARTH, Faul
APPLICANT: Muligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT PELLING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: US 04105492.6
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR PILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR PELING DATE: 2005-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 924;
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                            1496 CATTTATTTACACTCTT-GATTCTACAATGTAGAAAA 1531
                                                           CATTTATTTACACTCTTGGATTCTACAATGGTAGAAA 816
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Best Local Similarity 97.7%; Pred. No. 8.3e-133;
Matches 798; Conservative 0; Mismatches 14.
                                                                                                                                                                                              Sequence 137395, Application US/11266748A Ubblication No. US20060134663A1 GENERAL INFORMATION:
APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (152) ...(152)
; OTHER INFORMATION: n is a, c, g, or t
US-11-266-748A-137395
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NAME/KEY: misc feature
LOCATION: (103)...(103)
OTHER INFORMATION: n is a,
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LOCATION: (52)..(52)
OTHER INFORMATION: n is
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NAME/KEY: misc_feature
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LENGTH: 924
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND
TITLE OF INVENTION: METHODS FOR THEIR USE
FILE REFERENCE: 210121.428C7
CURRENT APPLICATION NUMBER: US/11/349,541
CURRENT FILING DATE: 1298-07-14
PRIOR PLING DATE: 1298-02-25
PRIOR PLING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-05
PRIOR FILING DATE: 1998-02-05
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1998-02-09
PRIOR FILING DATE: 1999-08-01
PRIOR PRIOR DATE: 1997-08-01
PRIOR APPLICATION NUMBER: US 08/904,809
PRIOR FILING DATE: 1997-02-05
PRIOR PRIOR DATE: 1997-02-05
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 74

LENGTH: 537
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                                                                   241 AAAGAATTACAGACTCTGATTCTACAGTGATGGATTGAATTCTAAAAATGGTAATCATTAG
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Best Local Similarity 98.5%; Pred. No. 2.1e-90;
Matches 529; Conservative 0; Mismatches 7;
                                         1456 AGTGAAAAGGAATGATATATTCTTGAAGACAT
                                                                                                                                                                                                                                                                                                                                                  Sequence 74, Application US/11349541; Publication No. US20060223129A1; GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or G
US-11-349-541-74
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ORGANISM: Homo sapien
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APPLICANT: Foy, Teresa M.

APPLICANT: Matanabe, Yoshihiro
APPLICANT: Madaleine Joy
APPLICANT: Madeleine Joy
APPLICANT: Madeleine Joy
APPLICANT: Dengy Ta
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TILLE REFERENCE: 2.011.427.23
CURRENT APPLICATION NUMBER: US/11/344,932
CURRENT APPLICATION NUMBER: 10/012,896
PRIOR PILING DATE: 2000-05-09
PRIOR PILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/895,814
PRIOR PILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: 09/882,911
PRIOR PILING DATE: 2001-05-09
PRIOR PILING DATE: 2001-05-09
PRIOR PILING DATE: 2001-05-09
PRIOR PILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/759,143
PRIOR PILING DATE: 2000-11-09
PRIOR PILING DATE: 2000-11-09
PRIOR PILING DATE: 2000-11-09
PRIOR PILING DATE: 2000-11-09
PRIOR PILING DATE: 2000-10-01
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ORGANISM: Homo sapiens
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LOCATION: 317, 430
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Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                  CR856058 DKFZp469F
BQ291482 AGENCOURT
BL25625 602975075
BM675180 UI-E-EJO-
BG298921 602381336
A1796120 WH22693.X
CR856120 DKFZp469L
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BG289079 602382457
BG373634 G233412.X
BG035606 602325670
CR76468 DKFZp469K
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AM771287 x846408 X
BQ26731373 x846408 X
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CSODJ007X107"
/tissue_type="T cells (Jurkat cell line) Cot
/plasmid="pcMVSPORT_6"
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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Query Match 96.9%; Score 1571; DB 6; Length 1967; Best Local Similarity 99.7%; Pred. No. 0; 5; Indels 0; Gaps 0; Matches 1574; Conservative 0; Mismatches 5; Indels 0; Gaps 0; 1 CGCATGGCATGCAGGCATCTCGGTCATGGAGCTGTCCGGCCTGGCCCGGGCCGTT 60 Indels 1	161 CCGCTACGACGTGTGTTGTGTGTTGTTTGTTGTTGTGTGTG	BAAGCTTCTGC BAAGCTTCTGC BAAAATTGGC CAAAATTGGC	421 TGGTGAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTCGCCTTAT 480 [941 TITTGAGGAGGTTGTTCATCATGATCACAAGGAGGGGCTCGTTATCACCAGTGA 1000 961 GGAGCAGGACGTGAGCCCCGGCCTTGCTGTTAAACACCCCAGCCATCCTTC 1020

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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1544)

1i, W. B., Gruber, C., Jessee, J., and Polayes, D.

Pull-length cDNA libraries and normalization
Unpublished
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1573 ATTTACACTCTTGATTCTACAATGTAGAAAATGAGGAAATGCCACAAATTGTATGGTGAT
GGAGCAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCCAGCCATCCCTTC
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 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK010Y111"
/tissue_type="HeLa cells Cc/plasmid="pcMvSPORT_6"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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full-length cDNA clone CS0DM013Y103 of Fetal liver
(human).
                                       GAAGGCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGA
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1 (bases 1 to 1598)

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     - Web : www.genoscope.cns.fr)
lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

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                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODIO27VJ12"
/tissue_type="Placenta Cot 2:
/plasmid="pcMvSPORT_6"
                                                                                                                                                                                                 Score 1532.6;
Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.7%;
Matches 1535; Conservative
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Bammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Pongo:
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CR857309
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Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecok V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Pred. No. 8.2e-313;
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkz-heidelberg.de;
sequenced by Qiaqen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
Rhis clone (DKF296901232) is available at the RZDD Deutsches
Reseaucrenzentrum fuer Genomforschung GmbH in Berlin, Germany.
Please contact RZDD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKRZp46901232
Further information about the clone and the sequencing project is
available at http://mipp.gsf.de/projects/cdna/.
Location/Qualifiers
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   Bahr, A., Lauber, J., Mewes, H.W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S. The German cDNA Consortium Direct Submission Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr. 1, D-85764
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Pred. No. 2.4e-293;
0; Mismatches 37; Indels
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Best Local Similarity 97.1%;
Matches 1416; Conservative
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EXPX cedex - FRANCE
Email: seqrefégenoscope.cns.fr. Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 977)

Li,W. Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
Unpublished (2001)

On Feb 15, 2001 this sequence version replaced on the contact: Genoscope
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.spenoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                       mRNA linear EST 23-APR-2004
25-NORMALIZED Homo sapiens cDNA
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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/mol_type="mRNA"
/db_xref="taxon:person"
/db_xref="taxon:person"
/db_xref="taxon:person"
/db_xref="taxon:person"
/clone="CSOIG62Y019"
/clone="Ibb="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
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                                                                                                                                                                                                                                                                                                                       Hominidae; Homo.

1 (bases 1 to 1042)

Li, W. B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)
On May 5, 2003 this sequence version replaced gi:30384374.
Contact: Genoscope
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                                                                                                         BX359836 mRNA BX359836 Homo sapiens PLACENTA COT 25-NORA clone CSODI062YO19 5-PRIME, mRNA sequence.
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Pred. No. 4.4e-197;
2; Mismatches 15;
    CTTATATTTTGAATGGGTT 1550
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94.8%;
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Homo sapiens
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AYBOUGHOU 1534 bp mRNA linear HTC 31-JAN-2005
Sus scrofa clone Clu_4587.scr.msk.pl.Contigl, mRNA sequence.
AY609940
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Hornshoj,H., Bendixen,C. and Panitz,F.
Direct Submission
Submitted (28-APR-2004) Animal Breeding and Genetics, Danish
Institute of Agricultural Sciences, Research Centre Foulum, Postbox
50, Tjele DK-8830, Denmark
                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        l (bases 1 to 1534)
Jorgensen, F.G., Hobolth, A., Hornshoj, H., Bendixen, C., Fredholm, M. and Schierup, M.H.
Comparative analysis of protein coding sequences from human, mouse and the domesticated pig
(er) BMC Biol. 3 (1), 2 (2005)
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                                                    GAGCATGGATGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCAAAGAC
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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="Clu_4587.scr.msk.pl.Contig1"
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Pred. No. 1.1e-192;
0; Mismatches 259;
                                                                                                                                                                                      934
                                                                                                                                                                                                         TTTTGAGGAGGTTGTTCATCATGATCACAACAAG
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                                                                                                                                                                                                                                     /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                                                          COT 10-NORMALIZED
      to sequence cluster
                                                                                                                                                              /cell type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZEI /cell line="TURKAT" /clone lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODJ007AE04QPl&c=2801.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                          Length 977;
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      division of Invitrogen. This sequence belongs
                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                        Score 916.4; DB 1;
Pred. No. 6.6e-193;
                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                      /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CSODJ007Y107"
                                                                                                                                                                                                                                                                                                                                          tch 56.5%; al Similarity 99.4%; 928; Conservative 2
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241 CTITION CONTRICTOR AND AND CONTRICTOR AND AND CONTRICTOR AND C		o No N	ΝS			venoscope - Centre National de Sequencage 2 rue Gaston Cremieur 5706 - 91657 EWY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI.oligo(dT) primer. Five prime	end enriched, double-strand cunA was digested with Not 1 and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized Library was constructed by Life Technologies, a division of Invitrogen.	This seque For more i http://www	Source / organism="Homo sapiens" /mol_type="mRNA" /db_txf="taxon:9606" //l=_e monawayaya	/clone_coursolatos /tissue_type="FETAL LIVER" /dev stage="fetal" /clone_lib="Homo sapiens FETAL LIVER"	Another and was primed with a Noticelly by the brime condensity of the prime and enriched, double-strand cDNA was digested with Not I and enriched into the Not I and Ecosy sites of the pCMVSPORT 6	y Match	Similarity 98.7%; Pred. No. 1.7e-186 7; Conservative 6; Mismatches 5 GTGGAGCACCTTTCTATACGACTTACAGGACAGCAGT	GIGGAGCACCTITCTATACSACTIACAGKACAGCAGATGGGGGAATTCATGGTGTTGTTGAG	855 CAATAGAACCCCAGTTCTACGAGCTGATCAAAGGACTTKGGACTAAAGGACTAGAAGAA 796	767 CTTCCCAATCAGATGAGTGGATGATTGGCCAGAAATGAAGAAGATGAGAAGTTTGCAGATGTA 826	827 TTTGCAAAGACGAAGGCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTG 886
21 CITCGGCGCGGGTGTGATGGAAACTCCAGCGGGGGAACTCTGCGGGGAAAAACTCCAGCGGGGGGGG	00 Aq	RESULT BX44900 LOCUS DEFINIT ACCESSI VERSION	KEYWOK SOURCE ORGA	REFER	COMMENT			FEATURES				ORIGIN	Bes Mat	3 A 8	S 8	\dot \d	& a
21 CITCGGCGCGGGTGTGATGGAAACTCCAGCGGGGGAACTCTGCGGGGAAAAACTCCAGCGGGGGGGG						e											
	CTTCCGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAAA	AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAATTGGCAGAAG 	GTGTGCACTGGGCATTATAATGGCTCTTTTTGACCGCACGCA	CATTGATGCAAATATGGTGGAAGGAACGCATATTAAGTTCTTTTCTGTGGAAAACTCA 	GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT	CTATACGACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 	GTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCCATCAGAT	GAGCATGGATGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTGCAAAGAAGA 	GAAGGCAGAGTGGTGAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGAC 	TITIGAGGAGTIGITCATCATGATCACAACAAGGAACGGGGCTCGTITATCACCAGTGA	GGAGCAGGACGTGAGCCCCCGCCCTGCACCTCTGCTGTTAAACACCCCAGCCATCCCTTC	TITCAAAAGGATCCTITCAIAGGAGAACACACTGAGGAGATACTIGAAGAAIITGGAIT 	CAGCCGGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAA 	AGCTAGTCTCTAACTTCCAGGCCCACGCTCAAGTGAATTTGAATACTGCAT	3 TTACAGGGTAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	TTACAGTATAGTGTAATGCAGAAAATCGTATGCATAGAAACGAGAGAAAAAAATATCAC AGTGTCCTACCACTCTAATCAAGAAAAAGAATTACAGACTCTGATTCTACAGGGAGATGATTG	

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end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                        /Lissue type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                             organism="Homo sapiens"
                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1027YJ12"
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Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime
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AL571115 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI027YJ12 3-PRIME, mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 971)

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Full.length cDNA libraries and normalization

Unpublished (2001)
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Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Consocope - Centre National de Sequencage
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVBORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
 1391
                                                                    CTTCCAGTTTGCTTGATATTTGTTGATATTAAGATTCTTGACTTATATTTTGAATGGG 1451
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AL545355 Homo sapiens PLACENTA COT 25-NRMALIZED Homo sapiens CDNA clone CSODI027YJ12 5-PRIME, mRNA sequence.
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/mol_type="mRNA"
/db_xref="taxon:9806"
/clone="CONORYSI2"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 TTAGGGCTTTTTGATTTATAAAACTTTTGGGTACTTATATAATTATGGTAGTTATTCTGC
                  TTAGGGCTTTTGATTTATAAAACTTTGGGTACTTATACTAAATTATGGTAGTTATTCTGC
                                                                                      CTTCCAGTTTGCTTGATATTTGTTGATATTAAGATTCTTRACTTATATTTTGAATGGG
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1 (bases 1 to 1081)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
Unpublished (2001)
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S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Clone distribution: MGC clone distribution information can be http://image.llnl.gov
Plate: LLAM10630 row: f column: 12
High quality sequence stop: 805.
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/lab host="hH10B (T1 phage-resistant)"
/lab host="organ: skin, Vector: pcMV-SPORT6; Site 1: Not1;
Site 2: Sall; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo.

The initial of to 1076)

Statement of the constant of the contract; Genoscope - Centre National de Sequencage

Contact: Genoscope - Centre National de Sequencage

Contact: Genoscope - Centre National de Sequencage

Contact: Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Ist strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a davision of Invitrogen. This sequence belongs to sequence cluster
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/note="let strand cDNA was primed with a Not1-oligo(dT)
primer: Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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/clone="CSOBKO10Y111"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
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Matches 816; Conservative
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Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
GTGTGCACTGGGCATTATAATGGCTCTTTTTGACCGCACACGCACTGACAAGGGTCAAGT 552
                                                                                                               GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT 660
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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/tisue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
Choroid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae, Homo.

1 (bases 1 to 823)

Bonaldo, M.F., Lennon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene
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UI-E-EJO-aig-n-09-0-UI.rl UI-E-EJO Homo sapiens CDNA clone
UI-E-EJO-aig-n-09-0-UI 5', mRNA sequence.
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Coordinated Laboratory for Computational Genomics
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BM723657.1 GI:19044988
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BM723657
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host="DH10B (Life Technologies) (T1 phage resistant)'
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0; Mismatches 7;
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 Db
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Db 781 GTAGTTATTCTGCCTTCCAGTTTGCTTGATATTTGTTGATA 823

Search completed: December 31, 2006, 19:30:55 Job time : 12999.5 secs

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AUTHORS
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AR237203 Sequence
AR27203 Sequence
AR370819 Sequence
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AR370819 Sequence
AR370819 Sequence
AR405226 Sequence
AR4139430 Sequence
AR56360 Sequence
AR56512 Sequence
AR65412 Sequence
AR65712 Sequence
AR65712 Sequence
AR6571 Sequence
AR657026 Sequence
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                                                                                            December 31, 2006, 12:13:09; Search time 10436.3 Seconds (without alignments) 9932.518 Million cell updates/sec
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                                                                                                                                                                                Description
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             GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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AR392324
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AR588592
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PF 25-FEB-1998 UP 1998537008
PR 25-FEB-1998 UP 1998537008
PR 25-FEB-1998 US 08/904809 PR 09-FEB-1999 US 08/904809 PR 09-FEB-1998 US 08/9020747
PI JIANGCHUN XU,DAVIN C DILLON
PC G01N33/574,G01N33/577,C07K16/30,A61K39/395,A61K47/48,C12Q1/68,CC G01N33/543
CC Topology: Linear;
CC Topology: Linear;
CC Compounds for immunodiagnosis of prostate cancer and methods
CC Topology: Linear;
CC FR for their use
CC Compounds for immunodiagnosis of prostate cancer and methods
CC Topology: Linear;
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BD070256 1621 bp DNA linear PAT 27-AUG-2002 Compounds for immunodiagnosis of prostate cancer and methods for Lhair use.
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 1621)

Xu,J. and Dillon, D. C.

Compounds for immunodiagnosis of prostate cancer and methods for
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C12N5/10,
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Lis,Xx., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of prostate
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        Xu,J., Dillon,D.C. and Mitcham,J.L.
Compounds for immunotherapy of prostate
their use
Patent: US 6465611-A 107 15-OCT-2002;
Corixa Corporation; Seattle, WA
Location/Qualifiers
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yuqiu,J.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and
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Patent: US 6129505-A 107 11-DEC-2001;
Corixa Corporation; Seattle, WA
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Patent: US 6512094-A 107 28-JAN-2003;
Corixa Corporation; Seattle, WA
Location/Qualifiers
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Conservative 0; Mismatches
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L.
Prostate specific fusion protein compositions
Patent: US 6395278-A 107 28-MAY-2002;
Corixa Corporation; Seattle, WA
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	RESULT 11 AR563606 LOCUS LOCUS DEPINITION Sequence 107 from patent US 6759515. ACCESSION AR563606 VERSION AR563606.1 GI:53978657 KEYWORDS INFORM	NISM ORS	cancer AL Patent: US 6759515-A 107 06-JUL-2004; Corixa Corporation; Seattle, WA S Location/Qualifiers urce /organism="unknown" /mol_type="genomic DNA"	y Match 100.0%; Score 1621; DB 2; Length 1621; Local Similarity 100.0%; Pred. No. 0; hes 1621; Conservative 0; Mismatches 0; Indels 0;		121 CCGCTACGACGCGCTTGGGCCGGGGCCACGCTCGCTAGTGCTGGACCTGAAGCA 	Db 181 GCCGCGGGGGGGCCCCTGCTGCTGCTGCAAGCGGTCGGATGTGCTGCAGGCC 240 Qy 241 CTTCCGCCGCGGTGTCATGGAGAAACTCCAGGTGGGCCCAGAGATTCTGCAGCGGAAAA 300 L	Oy 301 TCCAAGGCTTATTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTT 360
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	RESULT 12 ARS88592 LOCUST LOCUST SETULITION Sequence 107 from patent US 6800746. ACCESSION ARS88592.1 GI:S6635489 KENGION CORGE SOURCE ORGANISM Unknown. ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 1621)	AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A. TITLE Compositions and methods for the therapy and diagnosis of prostate cancer US 6800746-A 107 05-OCT-2004; Corixa Corporation; Seattle, WA FEATURES Location/Qualifiers location/Qualifiers /mol_type="genomic DNA"	ORIGIN Query Match Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 CGCATGGCACTCGGGCATCTCGGTCATGGGCTGCCCGGGCCCGGT 60 Db 1 CGCCATGGCACTCGGGGCATCTCGGTCATGGGCTGGCCCCGGGCCCGTT 60 Oy 61 CTGTGCTATGGTCGTCGGGGCGCTTGGGGCGCGGGCCGGCC		241 CTTCGGCGGGTGTCATGGAGAAACTCCAGCTGGGCCCAGAGATTCTGCGGGGGAAAA
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	13 12 12 TION ION ION DS	Unknown. Unknown. Unknown. Unclassified. Unclassified. SX Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y. Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H. Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W., Hepler,W.T. and Henderson,R.A.		11021 /organism="unknown" /mol_type="genomic DNA"	Query Match 100.0%; Score 1621; DB 2; Length 1621; Best Local Similarity 100.0%; Pred. No. 0; Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 1 CGCCATGGAGGCATCTGGAGGCTTGGAGCTGGCCCGGGGCCCGTT CGCCTTGGAGGCCTTGGAGGCTGGGCCCGGGGCCCGTT	1 61	DD 5.1 CIGIGATAGATCATGACTICAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	Qy 181 GCGCGGGGGGCGCGTGCTGCGGCGTCTGTGCAAGCGGTCTGGTGCTGCTGGAGGG Db 181 GCCGCGGGAGCCGCCGTGCTGCGGGCGTCTGTGCAAGCGGTCGGATGTGCTGCAGGGCC	Oy 241 CTTCCGCCGCGGTGTCATGGAGAAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAAA CTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAAA CTCCAGCTGGGGCCCAGAGATTCTGCAGCGGGAAAA	Oy 301 TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGGCTTCTGCCGGTT	361 A	421	Db 421 TGGTGAGAATCCGTATGCCCCGCTGAATCTCCTGGCTGACTTGCTGGTGGTGGCCTTAT
0y 421 TGGTGAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGTGGCTTAT 480 1	Qy 601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT 660	Qy 721 GTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT 780 Db 721 GTTCTACGAGCTGCTGATCAAAGGACTTGGACTAGATCTTGCAATGAACTTCCCAATCAGAT 780 Qy 781 GAGCATGGATGATTGGCCAGAAATGAAGAAGAAGAAGTGTATTTGCAAAAGAAGAC 840 Db 781 GAGCATGGATGGATTGGCCAGAAATGAAGAAGAAGAAGTTTGCAGATGTATTTGCAAAAGAAGAC 840	841 GAAGGCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGAC	OY 901 TITIGAGGAGGITGITCATCATGATCACAACAAGGACCICGITTATCACCAGIGA 960	961 GGAGCAGGACGTGACCCCCGCCCTGCACCTCTGCTGTTAAACACCCCCGGCCATCCCTTC 1021 TTTCAAAAGGGATCCTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATT 11		AGCTAGTCTCTAACTTCCAGGCCCACGGCTCAAGTGAATTTGAATACTGCATTTACAGTG 	01 TAGAGTAACACATACATTGTATGCATGGAAACATGGAGGAACAGTATTACAGTGTCCTA 	OY 1261 CCACTCTAATCAAGAAATTACAGACTCTGATTCTACAGTGATGATTGAATTCTAAA 1320	OY 1321 AATGGTTATCATTAGGGCTTTTGATTTATAAAACTTTGGGTACTTATACTAAATTATGGT 1380 	OY 1381 AGTTATTCTGCCTTCCAGTTTGCTTGATATATTTGTTGATATATAGATTCTTGACTTATA 1440 DD 1381 AGTTATTCTGCCTTCCAGTTTGCTTGATATTTGTTGATATTAAGATTCTTGACTTATA 1440	Qy 1441 ITTTGAATGGGTTCTAGTGAAAAGGAATGATATATTCTTGAAGACATCGATATACATT 1500 Db 1441 ITTTGAATGGGTTCTAGTGAAAAGGAATGATATATTCTTGAAGACATCGATACATT 1500	QY 1501 ATTTACACTCTTGATTCTACAATGTAGAAAATGAGGAAATGCCACAAAATTGTATGTGTGAT 1560

Db 1561 AAAAGTCACGTGAAACAAAAAAAAAAAAAAAAAAAAAAA	14 26 TION ION N DS	Unknown. ISM Unknown. Unclassified. CE 1 (bases 1 to 1621) RS Xu,J. and Dillon, D.C.	TITLE Compounds for immunodiagnosis of prostate cancer and methods for their use JOURNAL Patent: US 6887660-A 107 03-MAY-2005; Corixa Corporation; Seattle, WA FEATURES 10-01-10-10-11-11-11-11-11-11-11-11-11-1	/organism="unknown" /mol_type="mRNA"	UOTO WATCH 100.0%; SCOIE 1817, DB 2; DEMBLI 1817, Best Local Similarity 100.0%; Pred. No. 0; Matches 1621; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Ov 1 COCCATGACAGGCATCATGGAGGTCATGGAGGCTGGCCCGGGCCCGGGCCCGTT 60		61	Db 121 CGCTACGACGTGAGCTTGAGCTTGAGCGCTCGTAGTGCTAGTACTGAAGCA 180 Qy 181 GCCGCGGCGCGCCGCCTGCGCGCTCGTGCAAGCGATGTGCTGCTGCTGCTGCTAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGC	Db 181 GCCGCGGGAGCCGCCGTGCTGCGGCTCTGTGCAGCGGTCGGAATGTGCTGCAGCGGAGAA 200 Oy 241 CTTCGCCGGGGTGTCATGGAGAAATTCCAGCTGGGAAAA 300	Db 241 CTTCCGCCGCGGTGTCTTGAAAACTCCAGCGCCCAGAATTCTGCAGCGGAAAA 300 Oy 301 TCCAAGGCTTATTTATGCCAGGCTGAGTGGAGTTTGGCCAGGAAGCTTCTGCCGGTT 360	Db 301 TCCAAGGCTTATTTTTGCCAGGCTGGATTTGGCCAGFCAGGAGCTTCTGCCGGTT 360 Oy 361 AGCTGGCCAGATATTTGCCAGGTGTTCTCTCAAAATTGGCAGAAG 420	Db 361 AGCTGGCCACGATATCACTATTTGCCTTTGTCAGGTGTTCTCTCAAAATTGGCAGAAA 420 Qy 421 TGGTGAGAAACCGTGAACCTCCTGGCTGACTGTTGCTGGTGGCTTAT 480	Db 421 TGGTGAGAATCCGTATGCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGTGGCCTTAT 480 Ov 481 GTGTGCACTGGGCATTATAATGGCTCTTTTTGACCGCACACGCACTGACAAGGGTCAGGT 540	481 GTGTGCACTGGGCATTATAATGGCTCTTTTTGACCGCACACGGACTGACGAGGGTCAGG	QY 541 CATTGATGCAAAAGGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCA 600
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Sy B	781	GAGCATGGATGATTGGCCAGAAATGAAGAAGATTTGCAGATGTATTTGCAAAGAAGA 840
oy Dp	841	GAAGGCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGAC 900
δ qa	901	9 9
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ò q	1021	TITCAAAAGGATCCITTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGAIT 1080
δ qa	1081	CAGCCGCAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAA 1140
oy G	1141	0 0
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US-09-159-812-74	US-09-636-215-74	US-09-685-166A-74	US-09-115-453-74	US-09-688-489-74	US-09-679-426-74	US-09-759-143-74	US-09-651-236-74	US-09-030-606-74	US-09-657-279-74	US-10-012-896-74	US-09-116-134-74	US-10-144-678A-74	US-09-702-705-1504	US-09-736-457-1504	US-09-614-124B-1504	US-09-671-325-1504	US-09-658-824-1504	US-10-017-754-1504	US-09-651-563-1504	US-09-020-956-3	US-09-030-607-3
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31.8	31.8	31.8	31.8	31.8	31.8	31.8	31.8	31.8	31.8	31.8	31.8	31.8	26.3	26.3	26.3	26.3	26.3	26.3	26.3	25.1	25.1
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ALIGNMENTS

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Sequence 107, Application US/09020956
Patent No. 6261562
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956 FILING DATE: US/EB-1998 CLASSIFICATION:
                                                                                                                                                                                                                       3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
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US-09-020-956-107
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STRANDEDNESS: single
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CITY: Seattle
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Query Match
100.0%; Score 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches

CGCCATGGCACTGCAGGCATTCTCGGTCCATGCAGCTGTTCGGTCCCGGCCCCGTT 60 CGCCATGGCACTGCAGGCATTCTCGGTCCAGCTGTTCGTTTCTTCTTCTTTCT	1081 CAGCGCGAAGAGATTTATCAGCTTAACTCGGATAAATCATTGAAGTAAAT 1140 1081 CAGCGCGAAGAGATTTATCAGCTTAACTCGAATTCGAATTCGAATTATAACTCAGTTAA 1140 1081 CAGCGCGGAAGAGATTTATCAGCTCAAACTCGATTTACAGTG 1200 1141 AGCTAGTCCTCAACTTCCAGGCCCACGGCTCAAGTGAATTTGAATACTGCATTTACAGTG 1200 1141 AGCTAGTCCTCTAACTTCCAGGCCCACGGCTCAAGTGAATTTGAATACTGCATTTACAGTG 1200 1201 TAGAGTCACACATAACATTGAGCCACGGCTCAAGTGAATTTGAATATTACAGTG 1200 1201 TAGAGTAACACATTACAGCCACAGGCCAAGAGGAAACAGTATTACAGTGCCTA 1260 1201 TAGAGTAACACATAACATTGAGAACAGAACAGAACAGTATTACAGTGCCTA 1260 1201 TAGAGTAACACATAACATTGAGAACAGAACAGAACAGTATTACAGTGCCTA 1260 1201 TAGAGTAACAATAACATTATAACAACTCTCAACACACATTACAGTGCCTAA 1320 1201 TAGAGTAACAACAAAAAAAAAAAAAAAAACTTCGAATCAAAATTACAATTATAGA 1320 1201 AATTGGTTATCAGCGCTTTCATTAATAAAACTTTGAGATCATAAATTATGGT 1380 121 AATGGTTATCAGCGCTTTCATTAATAATAATTAAAAATTATCAAAATTATGGT 1380 121 AATGGTTATCAGCGCTTTCAGTTAATATAATAAAATTATGATTAAAATTATGGT 1380 121 AATGGTTATCAGCCTTTCAGTTAATATATAATAAAATTATCAAAATTATGGT 1380 122 AATGGTTATCTGCCAGTTGCTTGATAAATTTTTTTGAATCATTATTATAAAATTATGAATTATTATAAAATTATGAATTATT	SULT 2 -09-030-607-1C Sequence 107, Sequence 107, BAPLICANT: APPLICANT: APPLICANT: TITLE OF IN WOMBER OF SCHEETS: CITY: COUNTRY: ZIP: 981 COMPUTER RI MEDIUM TY TELEPHONI TELEPH
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APPLICANT: Miccham, Jennifer L.
APPLICANT: Miccham, Jennifer L.
APPLICANT: Jiang Yuqui
APPLICANT: Jiang Yuqui
APPLICANT: Jiang Yuqui
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Retter, Mark
APPLICANT: Retter, Mark
APPLICANT: Rolk, John
APPLICANT: Solk, John
APPLICANT: DIAGNOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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Patent No. 6329505
GENERAL INFORMATION:
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Pred. No. 0;
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            SEQUENCE CHARACTERISTICS:
LENGTH: 1621 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
                                                                                                                  ; ORGANISM: Homo sapiens
US-09-030-607-107
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Best Local Similarity 100.
Matches 1621; Conservative
 INFORMATION FOR SEQ ID NO:
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                                                                                           Sequence 107, Application US/09352616A
; Sequence 107, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Jiang, Yuqui
APPLICANT: Jiang, Yuqui
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: OP PROSTATE CANCER AND METHODS FOR THEIR USE
TITLE REPERENCE: 210121.42768
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT PILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 107
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larity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
 FILE REFERENCE: 210121.427C9
CURRENT PEDLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: EastSEQ for Windows Version 3.0
SEQ ID NO 107
LENGTH: 1621
                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-107
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; Sequence 107, Application US/09232149A
; Patent No. 6465611
; GRERRAL INFORMATION:
APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
TILLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; TILLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
; TILLE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILLIO DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1077
LENGTH: 1621
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              ; TYPE: DNA
; ORGANISM: Homo sapien
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LENGTH: 1621
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121	GARATCGAGTCTGTGGGAAGCACCTCGAGCACATGATGGATGG	1201 TAGAGTAACACATAACATTGTATGCATGGAAACATGGAAGGAA

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1141 AGCTAGTCTCTAACTTCCAGGCCCAAGTGAATTTGAATACTGCATTTACAGTG 1200	1381	OY 1501 AITTACACHICIANICIANACANI CANONANI CANONA	1621 A	RESULT 10 US-09-688-489-107 ; Sequence 107, Application US/09688489 ; Patent No. 6664377	; GENERAL INFORMATION: ; APPLICANT: Xu, Jiangchun ; APPLICANT: Dillon, Davin C. ; APPLICANT: Miccham, Jennifer Lynn	; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE ; TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE ; FILE REFERENCE: 210121.42702 ; CHIDERM ADDITION NIMBER: 118/09/688.489	CURRENT FILING DATE: 2000-10-13 NUMBER OF SEQ ID NOS: 338 SOFTWARE: FastSEQ for Windows Version 3.0 SOFTWARE: FastSEQ for Windows Version 3.0	; LEVETH: 1621 ; TYPE: DNA ; ORGANISM: Homo sapien its.09-688-489-107	OWE	CCATGGGACTGCAGGCATCTCGGTCATCGGCTGTTCCGGCCTGGCCCCGGGCCCGTT 60	61 CTGTGCTATGCTCCTGGCTGACTTCGGGCGCGTGTGGTACGCTGAACCGGCCCGGCTCTGCTACGTAACGCGTGAACCGGGCCGGCTCTGTTAGTTA	121 CCGCTACGACGCTTGGGCCGGGGCAAGCGCTCGCTAGTGCTGGACCTGAAGGA 122 CCGCTACGACGCTTGGGCCGGGGCAAGCGCTCGCTAGTGCTGGACCTGAAGGA 133 GCCCTACGACGCTTGGACCTTGGGCCGGGGCAAGCGCTTGGTAGTGCTGGACCTGAAGGA	
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CONTROL	1081 CAGCCGCGAAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAA 1141 AGCTAGTCTCAACTTCCAGGCCCACGGCTCAAGTGAATTTGAATACTGCATTTACAGTG	Db 1141 AGCTAGTCTCTAACTTCCAGGCCCACGGCTCAAGTGAATTGAATACTGCATTTACAGTG 1200 Qy 1201 TAGAGTAACACATAACATTGTATGCATGGAAACATGGAGAACAGTATTACAGTGTCCTA 1260	1201	1261 CCACTCTAATCAACAAAAGAATTACAGACTCTGATTCTACAGGATTGAATTCTAAA	1321 AATGGTTATCATTAGGGCTTTTGATTTATAAACTTTGGGTACTTATACTAAATTATGGT 	1381 AGTTATTCTGCCTTCCAGTTTGCTTGATATTTTGTTGATATTAAGATTCTTGACTTATA	1441 TTTGARGGGTCTAGTGAAAAGAATGATATATTCTTGAAGACATGGTATTTTTTGATGATGTTTTTTGAATGATGATTTTTT	1501 ATTTACACTCTTCACAATCTAGAAATGAGGAAATGCCACAAATTGTATGGTGAT	1561	OY 1621 A 1621 Db 1621 A 1621	NESULT 13 US-09-651-236-107 Sequence 107, Application US/09651236	GENERAL INFORMATION: ; APPLICANT: Xu, Jiangchun ; APPLICANT: Dillon, Davin C.	Harlocker, Susan L Jiang, Yuqui Henderser, Robert			APPLICANT: Wang, Aljun ; APPLICANT: Skeiky, Yasir A.W. ; APPLICANT: Hepler, William ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND	110N: 110N: 110N: 120121.42718C18 ATION NUMBER: US/09/651,236 DATE: 2000-08-29	; NUMBER OF SEQ ID NOS: 803 ; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 107 ; LENGTH: 1621	; TYPE: DNA ; ORGANISM: Homo sapien US-09-651-236-107
			CCGCTACGACGTGAGCCGCTTGGGCCGGGGCAAGCGCTCGCT	GCCGCGGGGGGCGCCCTGCTGCGCGCCTCTGTGCAAGCGGTCGGATGTGCTGCTGCTGGAGCCCCGGGGGGGG	CTTCCGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAAA 	TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTTTCCAGGAGGCTTATTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTT	AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAAG 	TGGTGAGAATCCGTATGCCCGGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTATTGGTGGAAATCCCTGGTGGTGGTGGTGGCCTTATTGGTGAGAATCTCCTGGCTGACTTTGCTGGTGGTGGTGGTGGTGTTAT	GTGTGCACTGGGCATTATAATGGCTCTTTTTGACCGCACCACGCACTGACAAGGGTCAGGT 	CATTGATGCAAATATGGGGGAAGGAACGGATATTTAAGTTCTTTTCTGTGGAAAACTCA 	GARATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTCT 	CTATACCACTTACAGGACAGCAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA 	GTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT 	GAGCATGGATGATTGGCCAGAAATGAAGAAGGATTTGCAGATGTATTGCAAAGAAGA 	GAAGGCAGAGTGGTGAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGAC 	TITIGAGGAGTIGITGATGATGACAAGAAGGAGGGGGGCTGGTTTATGACGGGGAGTGTTTATGAGTGTGTTTATGAGTGTGTTTATGAGGACGGGGGCTGGTTTATGAGGACGGGGGCTGGTTTATGACAAGGAAGG	GGAGCAGGACGTGAGCCCCCGCCTGCACCTCTGCTGTTAAACACCCCAGCCATCCCTTC	TITCAAAAGGGATCCTITCATAGGAGAACACACTGAGGAGATACTTGAAGAATITGGATT 	CAGCCGCGAAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAA

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OF PROSTATE CANCER AND METHODS 1260 1320 1320 1380 1380 1440 1440 1500 1560 1620 ATTACACTCTTGATTCTACAATGTAGAAATGAGGAAATGCCACAAATTGTATGGTGAT CCACTCTAATCAAGAAAAGAATTACAGACTCTGATTCTACAGTGATGATTGTAAA TTTTGAATGGGTTCTAGTGAAAAGGAATGATATATTCTTGAAGACATCGATATACATTT ATTTACACTCTTGATTCTACAATGTAGAAATGAGGAAATGCCACAAATTGTGTGTAT AGTTATTCTGCCTTCCAGTTTGCTTGATATTTTGTTGATATTAAGATTCTTGACTTATA CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAA AGCTAGTCTCTAACTTCCAGGCCCCACGGCTCAAGTGAATTTGAATACTGCATTTACAGTG TAGAGTAACACATAACATTGTATGCATGGAAACATGGAGGAACAGTATTACAGTGTCCTA AATGGTTATCATTAGGGCTTTTGATTTATAAAACTTTGGGTACTTATACTTATATGGT US-90-303-606-107

Sequence 107, Application US/09030606

Patent No. 6887660

GENERAL INFORMATION:
APPLICANT: Xu, Jaingchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF P.
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STATE: WA
COUNTRY: USA
ZIP: 98104
ZIP: 98104
COMPUTRY: USA
ZIP: 98104
ZIP: Patentin Release #1.0, Version #1.30
CUMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CUMPUTER: Patentin Release #1.0, Version #1.30
CUMPUTER: David: 25-FEB-1998
CUMBENT APPLICATION NUMBER: US/09/030,606
FILING DATE: 25-FEB-1998
CUMBENT APPLICATION NUMBER: US/09/030,606
FILING DATE: 25-FEB-1998
CUMBENT MAME: Maki, David J.
REGISTRATION NUMBER: 31,392

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                                                                                    TTTTGAGGAGTTGTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGA
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Patent No. 6894146
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Kang, Yuqui
APPLICANT: Kanger, Gary,
APPLICANT: Retter, Marc W.
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REFERENCE/DOCKET NUMBER: 210121.428C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 682-6031
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 1621 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Matches 1621; Conservative
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                                                                       THE THERAPY
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APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Rieiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, William
TITLE OF INVENTION: DIAGNOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C19
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 877
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 107
LENDRY 1621
                                                                                                                                                                                   DB 3;
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                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapien
US-09-657-279-107
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Sequence 21284, A
Sequence 21872, A
                                                                   December 31, 2006, 12:22:01; Search time 2591.16 Seconds (without alignments) 7716.790 Million cell updates/sec
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GenCore version 5.1.9
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US-09-1232-880-107

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ALIGNMENTS

APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23 ö Length 1621; 0; Indels DB 3; Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches NUMBER OF SEQ ID NOS: 934 SOFTWARE: FastSEQ for Windows Version 3.0 CURRENT APPLICATION NUMBER: US/09/759,143 CURRENT FILING DATE: 2001-01-12 US-09-759-143-107 ; Sequence 107, Application US/09759143 ; Patent No. US20020022248A1 Harlocker, Susan L. Jiang, Yuqui Henderson, Robert A. Kalos, Michael D. Xu, Jiangchun Dillon, Davin C. Mitcham, Jennifer L. Stolk, John A. Day, Craig H. Vedvick, Thomas S Carter, Darrick Fanger, Gary R. Retter, Marc W. Wang, Aijun ; TYPE: DNA ; ORGANISM: Homo sapien US-09-759-143-107 Li, Samuel INFORMATION SEQ ID NO 107 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: LENGIH:

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6300 Columbia Center, 701 Fifth Avenue
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,606
FILING DATE: 25-FEB-1998
CLASSIFICATION:
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Sequence 107, Application US/09030606
Patent No. US20020081580A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOUNDS FOR IM
TUTLE OF INVENTION: COMPOUNDS FOR IM
CORRESPONDENCES: 224
CORRESPONDENCE ADDRESS:
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STREET: 6300 CC
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STATE: WA
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Best Local Similarity 100.
Matches 1621; Conservative
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Patent No. US20020081680A1
GENERAL INPORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER;
FILE REFERENCE: 210121.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
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ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.428C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 107:
SEQUENCE CHARACTERISTICS:
LENGTH: 1621 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
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Pred. No. 0;
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Patent No. US20020090372A1
GENERAL INFORMATION:
APPLICANT: XU, Janagchun
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
TITLE OF INVENTION: MATHODS FOR THEIR USE
TITLE OF INVENTION NETHODS FOR THEIR USE
TITLE OF UNENTIONS TOWNERS: 1090/115,453B
CURRENT APPLICATION NUMBER: US/09/115,453B
CURRENT FILING DATE: 1998-07-14
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FASTESO FOR Windows Version 3.0
SEQ ID NO 107
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 107 LENGTH: 1621 TYPE. ...
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Best Local Similarity 100.0%;
Matches 1621; Conservative 0;
                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-822-827-107
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Publication No. US20020193296A1
GENERAL INPORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Aclos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Varier, Darrick
APPLICANT: Varier, Darrick
APPLICANT: Seeky, Yssir A.
APPLICANT: Hepler, William T.
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APPLICANT: Henderson, Robert A.
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                   Query Match
100.0%; Score 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches
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Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Uedvick, Thomas S.
APPLICANT: Carter, Darrick
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND FILE REFRENCE: 210121.427026
CURRENT APPLICATION UNUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 107
                                                                                                                                                                                                                                                                 Length 1621;
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Best Local Similarity 100.0%;
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APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: Houghton, Raymond L.
APPLICANT: Wowlil, Patricia D.
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
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APPLICANT: Foy, Teresa
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wandanabe, Moshihiro
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100.0%; Score 1621;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1621; Conservative 0; Mismatches
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; ORGANISM: Homo sapiens
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APPLICANT: Harlocker, Susan Louise
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APPLICANT: Ralos, Michael
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APPLICANT: Rede, Steven G.
APPLICANT: Retter, Mark
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APPLICANT: Solk, John
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THEF
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427D3
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEC ID NO 107
LENGTH: 1621
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Best Local Similarity 100.0%; Pred. No. 0;
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APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Robert A.
APPLICANT: Raines, Wichael D.
APPLICANT: Raines, Marc W.
APPLICANT: Raines, Marc W.
APPLICANT: Bay, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aiun A.
APPLICANT: Wang, Aiun Carter, Darrick
APPLICANT: Walliam T.
APPLICANT: Watenabe, Yoshihiro
APPLICAN
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                                       APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                          GENERAL INFORMATION
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US-10-144-678A-107
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294-025-10 ence 107,		3 B	721 GTTCTACAGGTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT 780 721 GTTCTACAGGCTGCTGATCAAAGGACTTGGACTTAAAGTCTGATGAACTTCCCCAATCAGAT 780
A 0		.	CACCANCCARTCATHOCOCCACAAATGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA
; APPLICANT: Xu, Jiangchun ; APPLICANT: Stolk, John A.		දි අ	GAGCATICATION CACAGAMATER CACA
	E THERAPY AND	ò	841 GAAGGCAGAGTGGTGTCAAATCTTTGACGGCACAGATGCCTGTGTGACTCCGGTTCTGAC 900
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER ; FILE REPREMENE: 210121.42702.		ପୁ	
; CORKENI AFFLICATION NUMBER: US/10/294,025 ; CURRENT FILING DATE: 2002-11-12 : NUMBER OF SEO ID NOS: 1038		δ	901 TTTTGAGGAGGTTGTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGA 960
; SOFTWARE: FastSEQ for Windows Version 3.0		Dp	901 TITIGAGGAGGIIGITCATCATCATCAACAAGGAACGGGGCTCGIITATCACCAGTGA 960
LENGTH: 1621; TYPE: DNA		Š	961 GGAGCAGGACGTGACCCCGCCCTGCACCTCTGCTGTTAAACACCCCCAGCCATCCCTTC 1020
; ORGANISM: Homo sapiens US-10-294-025-107		qq	961 GGAGCAGGACGTGAGCCCCCCCCCCTGCTCTGCTGAACACCCCCAGCCATCCCTTC 1020
100.0%; Score 1621; DB 7;	Length 1621;	ζŏ	1021 TTTCAAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGATTTGGATT 1080
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241	GAAAA	ò	
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361	AGAAG	ò	1501 ATTTACACTCTTGATTCTACAATGTAGAAATGAGGAAATGCCCACAAATTGTATGGTGAT 1560
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481.	CAGGT	ò	AAAAGTCACGTGAAACAAAAAAAAAAAAAAAAAAAAAAA
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Qy 541 CATTGATGCAAATATGGTGGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCA		장 옵.	1621 A 1621 1621 A 1621

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                                              GAGCATGGATGATTGCCCAGAAATGAAGAAGATTTGCAGATGTATTTGCAAAGAAGAC
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GENERAL INFORMATION: APPLICANT: Ku, Jiangchun; APPLICANT: Ku, Jiangchun; APPLICANT: Dillon, Davin C.
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                                                                      APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
TITLE BOF INVENTION: CANCER AND METHODS FOR THEIR
FILE REPERENCE: 210121.47704
CURRENT APPLICATION NUMBER: US/10/688,838
CURRENT FILING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 107
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100.0%; Pred. No. 0;
cive 0; Mismatches
                                    ; Sequence 107, Application US/10688838; Publication No. US20040141989A1; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 1621; Conservative
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CORGANISM: Homo sapiens
US-10-688-838-107
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US-10-688-838-107
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                                                                                                                                                      APPLICANT: Day, CRAIGH.
APPLICANT: Vedvick, Tonnas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.
TITLE OF INVENTION: PROSTAPE-SPECIFIC POLYPEPTIDES AND FUSION
TITLE OF INVENTION: PROSTAPETIDES THEREOF
FILE REPERENCE: 210121.427C31
CURRENT PELLON NUMBER: US 09/586,857
PRIOR PELLOATION NUMBER: US 09/536,857
PRIOR PELLOATION NUMBER: US 09/536,857
PRIOR APPLICATION NUMBER: US 09/439,313
PRIOR FILING DATE: 2000-05-27
PRIOR PELLOATION NUMBER: US 09/439,313
PRIOR FILING DATE: 1999-07-13
PRIOR PILING DATE: 1999-07-14
PRIOR PILING DATE: 1998-09-23
PRIOR PILING DATE: 1998-09-23
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 107
                Harlocker, Susan L.
Jiang, Yuqiu
Reed, Steven G.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
                                                                                                                                             Day, Craig H.
Vedvick, Thomas S
Carter, Darrick
Li, Samuel X.
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CORGANISM: Homo sapien
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1321 AATGGTTATCATTAGGGCTTTTGATTTATAAAACTTTGGGTACTTATACTAAATTATGGT 	1381 AGTTATTCTGCCTTCCAGTTTGCTTGATATTTGTTGATATTAAGATTCTTGACTTATA 1477 AGTTATTCTGCCTTCCAGTTTGCTTGATATTTGTTGATAAGATTCTTGACTTATA	1441 TITIGAAIGGGITCTAGIGAAAAGGAAIGAIAITATICTIGAAGACAICGAIAIACAITT 	1501 ATTTACACTCTTGATTCTACAATGTAGAAAATGAGGAAATGCCACAAATTGTATGGTGAT 	
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Abv21881 Human pro Abv27112 Human pro Aah13696 Human cDN

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Aac91303 Human pol Abv22733 Human pro Abv28442 Human pro Abv28544 Human pro Abv22620 Human pro

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Novel human prostate specific tumour protein and fragments - useful for detecting and treating prostate cancers.
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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         This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate cancers. (Updated on 25-MAR-2003 to correct PR field.)
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                                                                                                                                                                                                                           Polypeptides comprising immunogenic portions of prostate in a vaccine for the treatment of prostate cancer.
                                                                                                                                                                                                                                                                         Claim 3; Page 76-77; 130pp; English.
                                                       97US-00806099.
97US-00904804.
98US-00020956.
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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and isolated to the production proteins (I), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the progress are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate column the AMH9337 to AMH9344 and AAMO1115 to AAMO1318 represent
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The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The polygoucleotide is useful for detecting cancer. The polygoucleotide is useful for detecting cancer. The polygoucleotide is useful for detecting cancer. The prostate specific polynucleotide of the invention
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Carter D;
                                                                                                                                                                                                                                            Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
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ive 0; Mismatches
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                                                                                                                                                                              prostate cDNA sequence #107
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09-MAY-2000, 2000US-00568100.

13-JUN-2000, 2000US-00570737.

13-JUN-2000, 2000US-00593793.

27-JUN-2000, 2000US-00636215.

29-AUG-2000, 2000US-00657236.

06-SEP-2000, 2000US-00657279.

10-OCT-2000, 2000US-00657279.
CDNA; 1621
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AAS63555 standard;
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	601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACATGTTGGATGGTGGAGGACCTTT 660 601 GAAATCGAGTCTGTGGGAAGCACCTCGAGGACATGTGATGGTGGAGGTGGAGGACCTTT 660 601 GAAATCGAGTCTGTGGAACCACCAGGACAATGTGATGGTGGAGGCTCTTT 660 601 CTATACCACTTACAGGACACCAGAATCAAGCTTGTGATGGTGAACCCCCA 720 601 CTATACAGCTTACAGGACAACCAGAATCATGGACCTGTTGGACCAATCAGAT 780 721 GTTCTACGAGCTGCTGATCAAAGGACTTGGACTTGTGATGAACTCCCAATCAGAT 780 722 GTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAATCAGAAT 780 731 GACCATGGATTGATCAAAGGACTTGGACTAATCAAAGTCTGATCAAAGACTGAATCAGAT 780 732 GACCAGGAATTGACCACAAACAAAATCAAAGTCTGATGAATTTGCAAAGAACAAAGAATGAAT

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specific proteins and oligonucleotides that hybridise to a polynuc that encodes a prostate specific protein are useful for detecting presence or absence of a cancer or monitoring the progression the progression of a cancer, especially prostate cancer. AAH02422 to AAB74798 to AAB74821 and AAB74830 are sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly
                                                                                                                                                                           Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein; immunogen; cancer; prostate specific antigen; PSA; prostatic acid phosphatase; PAP; prostate specific membrane antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kalos MD;
Carter D;
Hural J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, RR, Retter MM, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA, PD, Houghton RL, Y De Bassolscv, Foy TM;
                                                                                                                                                   Prostate cancer therapy associated cDNA #107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prostate specific protein and its encoding treatment and diagnosis of prostate cancer.
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                                                                         CDNA; 1621
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04-OCT-2000; 2000US-00679272.
28-MAR-2001; 2001US-00822827.
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MCNEILL P D.
HOUGHTON R L.
Y DE BASSOLS C V.
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MITCHAM J L.
HARLOCKER S L
JIANG Y.
KALOS M D.
FANGER G R.
RETTER M W.
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DAY C H.
VEDVICK T S.
CARTER D.
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WANGA.
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HEPLERWT.
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           A 1621
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Li SX, Wang
Mcneill PD,
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prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence represents a prostate cancer therapy associated CDNA. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formet directly from the US patent office at
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                                                                                                     Novel polynucleotide encoding polypeptide comprising a portion of prostate tumor protein useful for inhibiting development of prostate cancer or for treating prostate cancer in a patient.
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ment of
                                                                                                                                                              The sequence is a human prostate tumour cDNA which encodes a part tumour protein. The DNA is useful for inhibiting the development prostate cancer or for treating prostate cancer in a patient
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The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a cDNA described in the invention
                                                    cancer; vaccine; cytostatic; immunostimulant;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                         Human F1-12 cDNA sequence SEQ ID NO 107.
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27-MAR-2000; 2000US-00536857.
29-MAY-2000; 2000US-00569100.
12-MAY-2000; 2000US-005970737.
13-JUN-2000; 2000US-00593793.
27-JUN-2000; 2000US-00605783.
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97US-00904804.
98US-00030607.
98US-00115453.
98US-00115453.
98US-00154812.
99US-00288946.
99US-00435616.
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                                                    Human; cancer; prostate
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RETTER M W.
STOLK J. A.
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VEDVICK T S.
CARTER D.
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HARLOCKER S L
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Kalos MD; Carter D;

RESULT 11
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The invention relates to a method of detecting prostate cancer by contacting a biological sample from a patient with: (a) a binding agent that binds to a polypeptide having an immunogenic portion of a prostate protein or its variant; (b) 2 oligomocleotide primers, where 1 of the oligomocleotides is specific for a DNA encoding the polypeptide of (a); or (c) an oligomocleotide probe specific for a DNA molecule encoding the polypeptide of (a). The method and polypeptides are useful for diagnosing, treating, particularly by immunocherapy, monitoring the progression, and inhibiting the development of prostate cancer in a patient. The polypeptides may be used to generate antibodies useful for the diagnosis and monitoring of prostate cancer. ABSSB10-ABSSB146
                                                                                          Detecting prostate cancer comprises contacting a sample with an agent capable of binding to a polypeptide with an immunogenic portion of a prostate protein, oligonucleotide primers or a probe specific for DNA encoding the polypeptide.
                                                                                                                                                                                                                    Claim 1; Page 59-60; 111pp; English.
                                               WPI; 2002-607662/65.
Xu J, Dillon DC;
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Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;

RESULT 13 ACC95091 ID ACC95091 standard; cDNA; 1621 BP.

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AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel prostate-specific proteins (PSP) and their coding sequences. The PSPs and their coding sequences are useful for stimulating an immune response in a patient, or for treating prostate cancer in a patient and for determining, detecting or diagnosing the presence of a cancer in a patient. The present sequence was used to
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Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
Moneill PD, Houghton RL, Vinals Y De BassolsC, Foy TW, Watanabe Deng T;
                                                                                                      human;
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                                                                                               prostate-specific protein; PSP; cancer; ss.
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100.0%; Pred. No. 0;
ative 0; Mismatches
                                                                         specific cDNA sequence SEQ
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29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
                                                                                                                                                                                                                                09-MAY-2002; 2002WO-US014753
                                                                                                      therapy; prostate
                                              (first entry)
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Matches 1621; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                     immune response;
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                                              28-AUG-2003
                                                                                                      Cytostatic;
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                                                                          Prostate
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                                                  1501 ATTTACACTCTTGATTCTACAATGTAGAAATGAGGAAATGGCCACAAATTGTATGGTGAT 1560
                                                                             Human; 88; prostate specific cDNA; cytostatic; immunostimulant;
gene therapy; call therapy; vaccine; T-cell epitope;
class I major histocompatibility complex allele; MHC; prostate cancer;
tumour; antigen presenting cell.
             ATTTACACTCTTGATTCTACAATGTAGAAAATGAGGAAATGCCACAAATTGTATGGTGAT
                                                                     Human prostate specific full length cDNA F1-12/P504S.
                                                                                                                                                  ADB13557 standard; cDNA; 1621 BP
                                                                                                                                                                                                                                                                                                            97US-00904804.
98US-00030607.
98US-00130607.
98US-00115453.
98US-00159812.
99US-00232149.
99US-00352616.
99US-00443686.
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2000US-00570737.
2000US-00593793.
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2000US-00636215
2000US-00651236
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2000US-00709729
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09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
                                                                                                                                                                                                                                               Homo sapiens.
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29-AUG-2000;
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09-NOV-2000;
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The invention relates to an isolated polypeptide comprising no more than CC The invention relates to an isolated polypeptide comprising a sequence ADB14487. The peptides comprise a fragment ADB1363 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MHC) alleles. ADB13653 is a polypeptide encoded by a human prostate specific CDNA, one of 648 disclosed as new. Also included are nucleic acids encoding the proteins and peptides, expression vectors, a host cell cTansformed with the vector, an isolated antibody (or antigen binding CT ransformed with the vector, an isolated antibody (or antigen binding GT fragment) that specifically binds to the protein or peptide, detecting the presence of a cancer in a patient (comprising contacting a patient sample with a binding agent that binds to the peptides or a polypeptide cappearing as ADB1355, detecting the amount of polypeptide that binds to off value to determine the presence of cancer), a fusion protein comprising the presence of acancer in a petient comprising the presence of cancer in a petient comprising administering a contacting T cells with the peptides or the isolated T cell population, treating prostate cancer in a patient and treating prostate cancer in a patient and treating prostate cancer in a patient and treating prostate cancer in a patient the T cells proliferate, and administering the cancer in a patient. The peptides or antigen presente of cancer in a patient. The peptides (or an incleic acids encoding, or muleic acids not cleic acids encoding them), is used to detect the captering calls proliferate, and administering che expressing the nucleic acids are used to cancer in a patient. The peptides, mucleic acids are seed to stimulate an immune response or treat presented thuman prostate specific connect in electronic format directing connect in a patient. The peptides or treat prostate cancer in a patient. The present sequence is one of the condicated, the sequence data for this patient endomediation or trea
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                                                                                                                          polypeptide for use in a vaccine for stimulating an in for treating or diagnosis cancer, preferably prostate
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100.0%; Pred. No. 0;
ive 0; Mismatches
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2003-756193/71
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                                           P-PSDB; ADB13558.
                                                                                                                          New isolated response, or
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CTTCCGCCGCGTGTCATGGAGAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAAA 300

Æ, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson F MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS; D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J; L PD, Houghton RL, Vinals Y De Bassolsc, Foy TM, Watanabe Deng T; Kalos MD, F Carter D, L Mcneill PD, Meagher MJ,

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2003-777973/73.

P-PSDB; ADG25974

polynucleotides encoding prostate specific polypeptides isolated iman prostate tumor cDNA library are useful to diagnose and treat cancer particularly prostate cancer New polyna human

Example 1; SEQ ID NO 107; 99pp; English.

The invention relates to human prostate-specific polypeptides and the polymucleotides encoding them. The invention also relates to an isolated antibody or its antiger-binding fragment that specifically binds a polypeptide of the invention, a method of detecting cancer in a patient comprising contacting a biological sample of the patient with an agent that binds a prostate-specific polypeptide and comparing the amount of bound polypeptide comparated to a predetermined cut-off value and a fusion protein comprising a prostate-specific polypeptide. The sequences of the invention are used to diagnose and treat cancer, particularly prostate cancer. This sequence represents cDNA encoding a human prostate-specific polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 1621 BP; 461 A; 330 C; 412 G; 418 T; 0 U; 0 Other;

ö 120 120 180 180 240 300 300 360 360 420 420 480 480 540 9 9 CTTCCGCCGCGGGTGTCATGGAGAAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAAA TCCAAGGCTTATTTATGCCAGGCTGAGTGGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTT AGCTGGCCACGATATCAACTATTTGGCTTTGTCAGGTGTTCTCTCAAAAATTGGCAGAAG CATTGATGCAAATATGGTGGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCA CGCCATGGCACTGCAGGGCATCTCGGTCATGGAGCTGTCCGGCCTGGCCCCGGGCCCGGTT CTGTGCTATGGTCCTGGCTGACTTCGGGGCGCGTGTACGCGTGGACCGGCCCCGGCTC CTGTGCTATGGTCCTGGCTGACTTCGGGGCGCGTGTACGCGTGGACCGGCCCCGGCTC GCCGCGCGCGCCCCCTGCCGCCTCTGTGCAAGCGGTCGGATGTGCTGCTGCTGGAGCC CTTCCGCCGCGGTGTCATGGAGAACTCCAGCTGGGCCCAGAGATTCTGCAGCGGGAAAA TCCAAGGCTTATTTATGCCAGGCTGAGTGGATTTGGCCAGTCAGGAAGCTTCTGCCGGTT TGGTGAGAATCCGTATGCCCCGCTGAATCTCCTGGCTGACTTTGCTGGTGGTGGCCTTAT GTGTGCACTGGGCATTATAATGGCTCTTTTTGACCGCACACGCACTGACAAGGGTCAGGT Grerecacresecarraraaresererrrrrgaceseacacacreacaagesreager DB 10; Length 1621; ö Indels . 0 ; Score 1621; I; Pred. No. 0; 0; Mismatches Query Match
Best Local Similarity 100.0%;
Matches 1621; Conservative 0; 241 61 61 121 121 181 181 241 301 301 361 361 421 421 481 481 541 g 셤 셤 셤 ò 음 상 음 8 8 8 ઠે 영 & g ઠે õ

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1380 1380 720 720 780 840 840 960 960 CTATACGACTTACAGGACAGCAGATGGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA GTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT GAAGGCAGAGTGGTGTCAAATCTTTGACGCACAGATGCCTGTGTGACTCCGGTTCTGAC TTTTGAGGAGGTTGTTCATCATGATCACAACAAGGAACGGGGCTCGTTTATCACCAGTGA TTTCAAAAGGGATCCTTTCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATT CAGCCGCGAAGAGATTTATCAGCTTAACTCAGATAAAATCATTGAAAGTAATAAGGTAAA AGTTATTCTGCCTTCCAGTTTGCTTGATATTTGTTGTTGATATTAAGATTCTTGACTTATA CATTGATGCAAATATGGTGGAAGGAACAGCATATTTAAGTTCTTTTCTGTGGAAAACTCA GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT GTTCTACGAGCTGCTGATCAAAGGACTTGGACTAAAGTCTGATGAACTTCCCAATCAGAT GAGCATGGATGATTGGCCAGAAATGAAGAAGAAGTTTGCAGATGTATTTGCAAAGAAGAC TITCAAAAGGGATCCTITCATAGGAGAACACACTGAGGAGATACTTGAAGAATTTGGATT AGCTAGTCTCTAACTTCCAGGCCCACGGCTCAAGTGAATTTGAATACTGCATTTACAGTG AGTIATICIGCCTICCAGITIGCTIGAIATATITIGITGAIATIAAGATICTIGACTIATA TITIGAATGGGTTCTAGTGAAAAGGAATGATATATTCTTGAAGACATCGATATACATTT ATTTACACTCTTGATTCTACAATGTAGAAATGAGGAAATGCCACAAATTGTATGGTGAT GAAATCGAGTCTGTGGGAAGCACCTCGAGGACAGAACATGTTGGATGGTGGAGCACCTTT CTATACGACTTACAGGACAGATGGGGAATTCATGGCTGTTGGAGCAATAGAACCCCA TAGAGTAACACATAACATTGTATGCATGGAAACATGGAGGAACAGTATTACAGTGTCCTA CCACTCTAATCAAGAAAGAATTACAGACTCTGATTCTACAGTGATGATTGAATTCTAAA **AATGGTTATCATTAGGGCTTTTTGATTAAAACTTTGGGTACTTATACTAAATTATGGT** A 1621 1081 1141 1201 1261 1321 1381 1021 1021 1081 1141 1201 1381 1441 1441 1501 1501 1,561 1621 541 721 781 781 841 841 901 901 196 961 1261 1321 601 601 661 661 721

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5.1.9 Biocceleration Ltd.	rch time 5186.18 Seconds ut alignmental modares/sec	ataaaaggggaccgt 647	es : 96473596			predicted by chance to have a score of the result being printed, octal score distribution. ARIES	A173209 nc22g03.x A473299 nc22g03.x A473298 nf51g01.x BF855163 RC3-FN020 BX096004 BX096004 A422513 nc22g03.r A425513 nc22g03.r AQ545351 CITBI-E1- A1734072 nc22g03.r AQ65921 CITBI-E1- AG183700 Pan trogal CG89163 Ygmt24306 AQ199998 RF0II-1-61 AQ171162 HS 3070 B AQ726978 HS 5213 B BF679787 602154577 BF679787 602154577 BF679598 np08902.8
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	37	51.2	7.9	394	7	BF368099	BF368099 CM3-GN004
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υ	40	49	7.6	300	7	BF368114	BF368114 CM3-GN004
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	43	46.8	7.2	836	σ	DN287707	DN287707 1242025 M
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ALIGNMENTS

AI732098 478 bp mRNA linear EST 14-JUN-1999 nc22g03.x5 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1008916, mRNA sequence. A1732098.1 GI:5053233 EST EST HOMO sapiens (human)	Bukaryota; Metazoa; Chordata, Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Mammalia; Homo, 1 (Bases 1 to 478) NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. Unpublished (1997) Email: Cancer Institute / National Institute of Dental Research, Contact: Robert Strausberg, Ph.D. Email: Capbs-romail.nih.gov Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:	This read is a RESEQUENCE of a previously sequenced human clone Original clone citation: WashU-NCI EST Project This read has been verified (found to hit its original self in the correct orientation) correct orientation) High quality sequence stop: 431. Location/Qualifiers Location/Qualifiers Location/Qualifiers And Lype="mRNA" Ab Arref="Laxon:9606" /clone="IMAGE:1008916"
RESULT 1 A1732098 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOUNCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	PEATURES

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Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.lgov/bbrp/image/image.html

Seq primer: -4nml3 fwd. ET from Amersham

High quality sequence stop: 367.
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Pred. No. 5.3e-112;
0; Mismatches 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
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ilarity 96.5%;
Conservative
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1 (Dases 1 to 461)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                          stage="45 years old"
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., G. Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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mRNA sequence.
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-FN0201-11100-011-f05&t3=2000-11-11&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 478.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
Tissue Procurement: W. Marston Linehan, Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Gree Lennon, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Gree Lennon, Ph.D.

CDNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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//folone_lone will primed with oligo(dfl) 70 50 mg of brand of the limed with oligo(dfl) 70 50 mg of brand total collular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was prostate to Eccal adaptors, 5 cycles of PCR applied to the CDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMPIO by the UDG-cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This read is a RESEQUENCE of a previously sequenced human clone original clone citation: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index This read has been varified (found to hit its original self in the
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                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                   Hominidae, Homo.

1 (bases 1 to 447)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  238 CTGCTAGAGAAAAGACCAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGGTA
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nf31g01.x5 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:915408 similar to contains element MSR1 repetitive element ;, mRNA
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0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              www-bio.lln1.gov/bbrp/image/image.html
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/lab_host="DH108"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:915408"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  correct orientation)
Insert Length: 621 Std Error: (Seq primer: -400P from Gibco High quality sequence stop: 423.
                                                                                                                                      AI732238.1 GI:5053351
                                                                                                                                                                                                      Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
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Matches 420;
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TITLE
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/dev stage="45 years old"
/lab_host="DH10B"
/lab_host="DH10B"
/clone lib="NCI CGAP Pr1"
/clone lib="NCI CGAP Pr1"
/note="Vector: pAMP10; Site=1: Not1; Site=2: EcoRI; lst strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the CDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCATCTTAAGGCAGCAGGACCAG
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                                                                                                    /db_xref="taxon:9606"
/clone="IMAGp998L052517 ; IMAGE:1008916"
                                                    organism="Homo sapiens"
Location/Qualifiers
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                                                                                                                                                    /sex="Male"
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Human UnigeneSet - RZPD3 (RZPDLIB No.972)
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
Http://www.rzpd.de/CloneCards/cgi-
bin/showibb.pl.cgi/response?libNo=972 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Indinindae; Homo.

1 (Dases 1 to 447)
Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Human UnigeneSet - RZPD3
Unpublished (2003)
Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenhaimer Feld 580, D-69120 Heidelberg, Germany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                          Length 480;
                                                                                                       Indels
                                                                                                            23;
                                                       Score 373.8; DB 2;
Pred. No. 9.7e-101;
0; Mismatches 23;
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                                                                                                            444; Conservative
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AUTHORS
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AQ545351 541 bp DNA linear GSS 28-MAY-1999 CITBI-E1-2613A22.TF CITBI-E1 Homo sapiens genomic clone 2613A22, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
70 GTGGCAACAATGCAGCAGCAGAATCAAT-GAAACAACAGAATGATTGCAATCATTCTGTT 12
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="sperm"
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/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 GGTGCCTCACAGTAGATCTGGTAGCAAAGAAGAAGAACAACACTGATCTCTTTCTG
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGPP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bo.llnl.gov/bbpyimage/image.html
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stops 367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="45 years old"
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/lab_host="minoB"
/clone_lib="NCI_CGAP_Prl"
/clone_lib="NCI_CGAP_Prl"
/note="Vector: plane1"; Site_1: Not1; Site_2: EcoRI; lst
strand_cDNA was primed with oligo(d7)7 on 50 mg of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected, histologically normal
prostate epithelial cells. Double-stranded cDNA was
ligated to EcoRI adaptors; S. cycles of PCR applied to the
CDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
constructed by David Krizman."
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                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        485 GATCTGGTAGCAAAGGAAGAAGAAACAAACAACGATCTTTTTTGCCACCCCTCTGACCC
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94.8%; Pred. No. 1.8e-96;
live 0; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:1008916"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="Male"
                                                           Tumor Gene Index
Unpublished (1997)
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Best Local Similarity 94.8
Matches 458; Conservative
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AQ469231 546 bp DNA linear GSS 23-APR-1999 CITBI-E1-2601M18.TF CITBI-E1 Homo sapiens genomic clone 2601M18, genomic survey sequence.
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Mls-21
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                             399 AAGCCTACCTAATATCTGCTAGAGAAAAGACCAACAAC-GCCTCAAAGGATCTCTTACCA 341
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGAAGGGTCAATTTGCTCATTTTGTGTGTGAAAAGTCAGGATGCCCAGGGGCCAGAG
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                                                                                                                                                                                                                                                                                                       223 AAGCCTACCTAATATCTGCTAGAGAAAAGACCAACAACGGCCTCAAAGGATCTCTTACCA
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1 (bases 1 to 546)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H.,
Venter,J.C.
                                                                             Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Map Building
Unpublished (1997)
Unpublished (1997)
Cother_GSSs: CTBI-E1-2601M18.TR
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0200
                                                                                                                                      Indels
                                                                                Score 355; DB 1;
Pred. No. 4.3e-95;
0; Mismatches 20;
constructed by David Krizman."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            583 AAACAACAGAATGATTGCAATGTCCTTTTTTT 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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AQ469231.1 GI:4653121
                                                                             55.0%;
ilarity 93.8%;
Conservative
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nes 425; Conserv
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Other ESTs: no22403.x5
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI734072 456 bp mRNA linear EST 14-JUN-1999 nc22g03.y5 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:1008916, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This read is a RESEQUENCE of a previously sequenced human clone Original clone citation: WashU-NCI EST Project
This read has been verified (found to hit its original self in the
                                     CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT 360
                                                                                                                                                                                                                                                                                   432 CACTTTGTGTGCGGATAAAGACAGGATGCCCAGCGGCCAGAGCAGGGTGCTG-GTGCTTT 490
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1 (bases 1 to 456)

NCI/NIDR-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Dental Research,

Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
        CTAGAGAAAAGACCAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300
                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                            CATITIGIGIGIGGATAAAGTCAGGATGCCCAGGGGCCAGAGCAGGGGGCTGCTTT
                                                                                                                                                                                                                                                                                                                                            465
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/lab_host="DH108"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Seg primer: -40RP from Gibco
High quality sequence stop: 422.
Location/Qualifiers
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Homo sapiens
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AI734072/c
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VERSION
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AUTHORS
TITLE
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(E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CG891636 1inear GSS 01-SEP-2004 Ygmt24306 Yunnan snub-nosed monkey genomic BAC library Pygathrix bieti genomic clone 24306, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 CCAGCGAAAAGACCAACA---GTTTCAAAGGATCTCTTACCATGAAGGCCTCAGTTAATT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCATCATAAGGCAG 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 ACAATITITCATIATCATGTAAATCAAATCACCCAAGGGGCCAACCACCACCAC
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                                                                                                                                                                                                                                                                                                                                                         /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                  52.0%; Score 335.8; DB 14; Length 713; larity 82.1%; Pred. No. 3e-89; Conservative 0; Mismatches 83; Indels 18;
Yokohama,
                                                                                                                                                                                                                                          1. 713
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db xref="taxon:9598"
/clone="RP43-057E05.TJ"
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                                                                                                                                                                    : pBACe3.6
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                                                                                                                                Sequencing: TJ
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R.Site 2
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Matches 463; Conserv
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Pan troglodytes DNA, clone: RP43-057E05.TJ, genomic survey
sequence.
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           /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
/db_cref="2601M18"
/sex="male"
/cell type="sperm"
/clone lib="CTTBLE1"
/note="Vector: pBeloBAC11; Site_1: ECORI; Site_2: ECORI;
Calfech Human BAC Library D"
                                                                                                                                                                                                                                                                                                                                                                           TGCTCAGGGGAAGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                      138 TGCT-TGGGGAAGGCTCATATGGGACTTTCTACTGCCTAAGGTTCTACACGATATAAA
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
Unpublished
                                                                                                                                                                                                                                                               10;
                                                                                                                                                                                                                      Score 353.8; DB 11; Length 546; Pred. No. 1.1e-94; 0; Mismatches 33; Indels 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGAACAATGGCTGAGCGTATAAGCATAGGTAAGG 523
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GSS.
                                                                                                                                                                                                                      Query Match 54.8%;
Best Local Similarity 90.6%;
Matches 413; Conservative (
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AQ199998 RPCI11-61C21.TK RPCI-11 Homo sapiens genomic clone RPCI-11-61C21,
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                                                                                                                                                                                                                                                                                          Hominiata, Mono.

1 (bases 1 to 481)

Madans, M.D., Rounaley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, B., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)

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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200

Fax: 301 838 0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                         Eukaryota; Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGAAAAGACCAACAACAACCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 ATTITICATIATCATGIAAATCACATCACTCAAGGGGCCAACCACACGTGGGAGCCACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 GAGAAAAGACCAACAACGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATTCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/noce="Vector: pBACe3.6; Site_1: EcoRI; Site_2:
RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
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GTATGACTTGCCATGAAGACTTGAGGACTCTGAATCAGTAAGGGCATCTT
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Pred. No. 3.6e-78;
0; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic_DNA"
/db_xref="GDB:7523108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="RPCI-11-61C21"
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                                                                                                                                          genomic survey sequence.
                                                                                                                                                                            AQ199998.1 GI:3612197
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Best Local Similarity 89.6%;
Matches 346; Conservative C
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                                                                                                                                                                                                                     Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Skin"
/cell type="Fibroblast"
/cell type="Fibroblast"
/cell type="Fibroblast"
/cell tine="KRD96009"
/clone_lib="Yunnan snub-nosed monkey genomic BAC library"
/note="Nector: pBACe3.6; Site_!: EcoRI; Genomic DNA was
partially digested with EcoRI_Vector, pBACe3.6.
Recombinants were transformed into DH10B."
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                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecidae; Colobinae; Pygathrix.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2003)
Contact: Xu, H.L.; Su, B.
Contact: Xu, H.L.; Su, B.
Key Laboratory of Cellular and Molecular Evolution
Kunming Institute of Zoology, the Chinese Academy of Sciences
32 Jiaochangdonglu, Kunming, Yunnan 650223, People's Republic China
Email: xuhl@mail.kiz.ac.cn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"

Retrain="Yunnan snub-nosed monkey"

(db_txef="taxon:61621"

/clone="24306"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48.5%; Score 313.6; DB 12;
83.8%; Pred. No. 1.3e-82;
iive 0; Mismatches 61;
                                                                Pygathrix bieti (black snub-nosed monkey)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .533
/organism="Pygathrix bieti"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                          GI:51792549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="male"
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Class: BAC ends.
                                                                                 Pygathrix bieti
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394; Conserv
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AQ726978 578 bp DNA linear GSS 14-JUL-1999
HS_5416_B2_F06_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic_clone Plate=992 Col=12 Row=L, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
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//note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI;
Male blood DNA was isolated from one randomly chosen donor and partially disested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites"
                                                                                                                                             457
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University of Mashington
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: juallaceeu, washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D.
                                        CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT
                 CTAGAGAAAAGACCAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT
                                                                                                                                             398 CITAGCIAAGAIGIGGGIICCACAIIAIGCICIGAAIACAGGAGGAAGGCICAAICIGCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 10449764
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=992_Col=12_Row=L"
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/organism="Homo sapiens"
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Class: BAC ends
High quality sequence stop: 578.
Location/Qualifiers
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Plate: 992 row: L column: 12
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                                                                                                                                                                                          361 CATTITGIGIGIGGAT 376
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il Similarity 82.6%;
314; Conservative (
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AQ726978
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hominidae, Homo.

1 (bases 1 to 474)

Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,

Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                      GGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGCGGNGAAGGGTCAATTTGGTCAC 455
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GGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGAAGGGTCAATTTGCTCAT 363
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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High Throughput Sequencing Center
Niversity of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3070 row: D column: 17
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Pred. No. 3.5e-76;
0; Mismatches 29;
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/db_xref="taxon:9606"
/clone="Plate=3070 Col=17 Row=D"
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                                                                              TTTGTGTGTGATAAAGTCAGGATGC 389
                                                                                                         High quality sequence stop: 474. Location/Qualifiers
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AQ171162.1 GI:3568529
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Best Local Similarity 89.9%;
Matches 338; Conservative
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Gontact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3687
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 809 row: N column: 4
Seq priner: 8P6
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1 (bases 1 to 407)
Mahairas, G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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                                                                                                                         CCAC-----ATTATTAGAACACCCTCTGACCCTTTATAACAAGCCCACCCCATATCTG 397
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ACGATTTTCATTATCATGTGAATCAGATCACTCAAGGGGCCAACCACAACTGGGAGCCAC 225
                                                                   TGAT-AGGGGAAGGCTCATATGGGACTATCTACTGCCTAAAGTTCAACACACAGAAATAAA 284
                                                                                                                                                                                                                                                                                                                                      and
                                                                                                       Sequence-tagged connectors: A sequence approach to mapping scanning the human genome

Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="plate=809 Col=4 Row=N"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                           AQ598346.1 GI:5029558
GSS.
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Homo sapiens
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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Best Local Similarity 86.2%;
Matches 294; Conservative
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Sequence 27951, A Sequence 552, App Sequence 552, App Sequence 552, App Sequence 552, App Sequence 552, App

Sequence

Sequence 552, App Sequence 14, Appl

Sequence 1161369, Sequence 587040, Sequence 1200449,

Sequence

Sequence 893115, Sequence 893115, Sequence 721218, Sequence 721218, Sequence 489987, Sequence 489987,

Sequence 241350, Sequence 241351, Sequence 241352

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Run on:

Sequence:

Searched:

us-09-232-880-308.rnpbm

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APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND FITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210.121.427023
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 647;
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6 US-10-301-480-547960
2 US-10-301-480-151369
2 US-10-301-480-1200449
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US-09-925-065A-721218
US-09-925-065A-489987
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US-10-357-930-274604
US-10-357-930-27951
US-09-759-143-552
US-09-822-827-552
US-09-895-793-552
US-10-895-793-552
US-10-10-895-552
US-10-012-896-552
US-10-012-896-552
US-10-294-625-552
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US-09-759-143-308
US-09-759-143-308
Sequence 308, Application US/09759143
Patent No. US2002202248A1
GENERAL INFORMATION:
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OTHER INFORMATION: n = A, T, C or G
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Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Dillon, Davin C.
Mitcham, Jennifer L.
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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ORGANISM: Homo sapien
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                | FBMC Celerra SIDS3/ptodata/2/pubpna/USO7 PUBCOMB.seq:*
| FBMC Celerra SIDS3/ptodata/2/pubpna/USO8 PUBCOMB.seq:*
| FBMC Celerra SIDS3/ptodata/2/pubpna/USO8 PUBCOMB.seq:*
| FBMC Celerra SIDS3/ptodata/2/pubpna/USO8 PUBCOMB.seq:*
| FBMC Celerra SIDS3/ptodata/2/pubpna/USO9 PUBCOMB.seq:*
| FBMC Celerra SIDS3/ptodata/2/pubpna/USO6 PUBCOMB.seq:*
                                                                                                                                                                                                                         December 31, 2006, 12:22:01; Search time 1030.23 Seconds (without alignments) 7716.790 Million cell updates/sec
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Sequence 21562,
Sequence 21578,
Sequence 22089,
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Sequence 21476,
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Sequence 308,
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                                           GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-357-930-21562
US-10-357-930-21578
US-10-357-930-22089
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US-09-780-665-308
US-09-822-887-308
US-09-212-880-308
US-09-895-793-308
US-09-895-793-308
US-10-0112-895-308
US-10-0112-895-308
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US-10-294-025-308
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Maximum Match 100%
Listing first 45 summaries
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Result No.

Best Local Matches 64

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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
                                                                                                                                                                                                                                                                      Length 647;
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                                                                                                                                                                                                                                                                    100.0%; Score 646; DB 3; L 100.0%; Pred. No. 2.7e-201; tive 0; Mismatches 0;
      COMPOSITIONS AND METHODS FOR DIAGNOSIS OF PROSTATE CANCER
    ; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CA;
; FILE REPERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: U$/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 308, Application US/09822827
; Sequence 308, Application US/09822827
; Patent No. US20020081680A1
; APPLICANT: Xv.
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                                                                                                                                                                                                        // LOCATION: (1)...(647)
// OTHER INFORMATION: n = A,T,C or
US-09-780-669-308
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Best Local Similarity 100.
Matches 647; Conservative
                                                                                                                                                                            FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)... (647)
                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapien
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            2.7e-201;
            Pred. No. 2.7
Mismatches
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Patent No. US20020051977A1
GENERAL INFORMATION:
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Hepler, William
Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas S
Carter, Darrick
Li, Samuel
                            647; Conservative
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              Similarity
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// LOCATION: (1)...(647)
// OTHER INFORMATION: n = A,T,C or G
US-09-232-880-308

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                                                                                                                                                         NAME/KEY: misc feature
                                                                                                                 TYPE: DNA
ORGANISM: Homo sapien
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US-09-895-793-308
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                                                                                                                                                                                                           Query Match
100.0%; Score 646; DB 3; L
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0;
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFREENCE: 210121.53401
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SEQ ID NO 308
LENGTH: 647
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
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                                                                                                                                                         ; LOCATION: (1)...(647)
; OTHER INFORMATION: n = A,T,C US-09-822-827-308
                                                                                                                                           NAME/KEY: misc_feature LOCATION: (1)...(647)
                                                                                                                  ORGANISM: Homo sapien
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US-09-232-880-308
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61 TGCTCAGGGGAAGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR FILE REFERENCE: 210121.42866 CURRENT APPLICATION NUMBER: US/09/232,880 CURRENT PILING DATE: 1999-01-15 NUMBER OF SEQ ID NOS: 338 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 646; DB 3; I Best Local Similarity 100.0%; Pred. No. 2.7e-201; Matches 647; Conservative 0; Mismatches 0;
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541 GGACCAGTTTGAGTGGGAACAATGCAGCAGAGAATCAATGGAAACAACAGAATGATTGC 600
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Houghton, Robert A.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Fonger, Gary R.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
ITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
ITILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT PILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 308
LENGTH: 647
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Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0;
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. Sequence 308, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
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NAME/KEY: misc feature

LOCATION: (1)...(647)

OTHER INFORMATION: n = A,T,C or G
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                                                                                                  APPLICANT: Retter, March W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Houghton, Raymond L.
APPLICANT: Winals de Bassols, Carlota
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Panger, Gary R.
APPLICANT: Panger, Gary R.
APPLICANT: Ponger, Gary R.
APPLICAN
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; OTHER INFORMATION: n = A,T,C or G
US-09-895-793-308
                            Harlocker, Susan L.
Jiang, Yugiu
Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
        Mitcham, Jennifer L.
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NAME/KEY: misc_feature
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ORGANISM: Homo sapien
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US Application US/10010940

Publication No. US20030088062A1

GENERAL INFORMATION:

APPLICANT: Willon, Davin C.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan Louise

APPLICANT: Hearlocker, Susan Louise

APPLICANT: Reed, Steven G.

APPLICANT: Read, Steven G.

APPLICANT: Retter, Machael

APPLICANT: Retter, Mark

APPLICANT: Banger, Gary

APPLICANT: Day, Craig

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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                                                                                                                      Length 647;
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                                                                                                                        100.0%; Score 646; DB 6; 1
100.0%; Pred. No. 2.7e-201;
ive 0; Mismatches 0;
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 123
; OTHER INFORMATION: n = A,T,C or
US-10-012-896-308
                                                                                                                    Query Match
Best Local Similarity 100.'
Matches 647; Conservative
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US-10-010-940-308
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    CCACCCCTCTGACCCTTTGGAACTCCTCTGACTCTTTAGAACAAGCCTACTAATATCTG
                                                                                  CTAGAGAAAAGACCAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT
                                                                                                       CTAGAGAAAAAGGCCAACAAAGGGTCTCTTACCATGAAGGTCTCAGCTAATT
                                                                                                                                                                                       CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 201-12-10
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601 AATGTCCTTTTTTTTCTCCTGCTTCTGACTTGATAAAGGGGACCGT 647
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xu, Jiangchun APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Kalos, Michael D. APPLICANT: Kalos, Michael D. APPLICANT: Retter, Marc W. APPLICANT: Boy, Zraig H. APPLICANT: Day, Zraig H. APPLICANT: Vedvick, Thomas S. APPLICANT: Carter, Day Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang, Aijun
Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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ORGANISM: Homo sapiens
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LENGTH: 647
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Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels
FILE REFERENCE: 210121,427D3
CURRENT APPLICATION NUMBER: US/10/010,940
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FRASESQ for Windows Version 3.0
SEQ ID NO 308
LENGTH: 647
                                                                                                                          NAME/KEY: misc feature

LOCATION: (1)...(647)

CTHER INFORMATION: n = A,T,C or G

US-10-010-940-308
                                                                                       TYPE: DNA
ORGANISM: Homo sapien
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MS-10-144-678A-308

Sequence 308, Application US/10144678A

Publication No. US20030157089A1

GENERAL INPORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Sugan L.

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241 CTAGAGAAAAGACCAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300
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APPLICANT: HURAL, John
APPLICANT: HURALL, John
APPLICANT: HOUGHCON, Raymond L.
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Poy, Teresa M.
APPLICANT: Poy, Teresa M.
APPLICANT: Desg, TB.
APPLICANT: COURCER: USAND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICANT: USAND
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 308
LENGTH: 647
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100.0%; Score 646; DB 7; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: n = A,T,C or G US-10-144-678A-308
                                                       Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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Hepler, William T.
Jiang, Yuqiu
Henderson, Robert
Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 123
                                                                                                                                                                                               Wang, Aijun
                                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.
TITLE OF INVENTION: PROCYPEPTIDES THEREOF
FILE REFERENCE: 210121.42731
FILE REFERENCE: 210121.42731
CURRENT APPLICATION NUMBER: US/11/234,786
CURRENT FILING DATE: 2000-09-09
FRIOR FILING DATE: 2000-05-09
FRIOR FILING DATE: 2000-05-09
FRIOR PELICATION NUMBER: US 09/536,857
FRIOR FILING DATE: 2000-05-09
FRIOR APPLICATION NUMBER: US 09/433,672
FRIOR FILING DATE: 1999-11-13
FRIOR FILING DATE: 1999-11-13
FRIOR FILING DATE: 1999-07-13
FRIOR FILING DATE: 1999-07-13
FRIOR PELICATION NUMBER: US 09/352,616
FRIOR APPLICATION NUMBER: US 09/232,149
FRIOR PELING DATE: 1999-07-13
FRIOR PELING DATE: 1999-07-13
FRIOR PELING DATE: 1999-07-15
FRIOR PELING DATE: 1999-01-15
FRIOR PELING DATE: 1999-01-15
FRIOR PELING DATE: 1999-01-15
FRIOR APPLICATION NUMBER: US 09/159,812
FRIOR PELING DATE: 1999-01-15
FRIOR APPLICATION NUMBER: US 09/115,453
FRIOR PELING DATE: 1999-07-14
FRIOR APPLICATION NUMBER: US 09/030,607
FRIOR PELING DATE: 1999-02-25
FRIOR APPLICATION NUMBER: US 09/030,607
FRIOR APPLICATION NUMBER: US 09/030,007
                                                        TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCATCTTAAGGCAGCA
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; OTHER INFORMATION: n = A,T,C or G
US-11-234-786-308
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Jiang, Yuqiu
Reed, Steven G.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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ORGANISM: Homo sapien
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LENGTH: 647
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                             TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCATCTTAAGGCAGCA
                                                                                                          GGACCAGTTTGAGTGGCAACAATGCAGCAGCAGAATCAATGGAAACAACAGAATGATTGC
                                                                                                                                           GGACCAGTTTGAGTGGCAACAATGCAGCAGCAGAATCAATGGAAACAACAACAGAATGCTTGC
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CURRENT APPLICATION NUMBER: US/10/294,025
CURRENT FILING DATE: 2002-11-12
NUMBER OF SEQ ID NOS: 1038
SSCFTWARE: PASISEQ for Windows Version 3.0
SSC IN NO 308
LENGTH: 647
                                                                                                                                                                                                                                                     601 AATGTCCTTTTTTTTTTCTCCTGCTTCTGACTTGATAAAAGGGGACCGT 647
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Best Local Similarity 100.0%; Pred. No. 2.7e-201;
Matches 647; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 308, Application US/10294025
Publication No. US20030185830A1
GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or
US-10-294-025-308
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ORGANISM: Homo sapiens
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APPLICANT: Schlegel. Robert
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
FITTE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCM
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT APPLICATION NUMBER: 00/1765,276
PRIOR PELLING DATE: 2003-02-04
PRIOR PELLING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-03-16
PRIOR PELLING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-08
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                                                     GGNGCCTCACAGTATAGATCTGGTAGCAAAGAAGAAGAACAAAAACACTGATCTCTTTCTG
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Publication No. US20040259086A1
GENERAL INFORMATION:
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                                                                                                                1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCCAACCACCAGCTGGGAGCCAC
                                                                                                                                                 ACGATTTTCATTATCATGTAAAATCGGGTCACTCAAGGGGCCCAACCACGCTGGGAGCCAC
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; Publication No. UG20030185830A1
; GENERAL INFORMATION:
    APPLICANT: Xt. Jiangchun A.
    APPLICANT: Stolk, John A.
    TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
    TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
    FILE REFERENCE: 210121.427C29
    CURRENT APPLICATION NUMBER: US/10/294,025
    CURRENT FILING DATE: 2002-11-12
    NUMBER OF SEQ ID NOS: 1038
    SOFTWARE: REALSEQ for Windows Version 3.0
    SSOFTMARE: REALSEQ for Windows Version 3.0
    LENGTH: 2577
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                                                        Indels
100.0%; Score 646; DB 16;
100.0%; Pred. No. 2.7e-201;
ive 0; Mismatches 0;
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Pred. No. 4.5e-186;
0; Mismatches 8;
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Best Local Similarity 98.1%;
Matches 629; Conservative
                             Best Local Similarity 100.
Matches 647; Conservative
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        FILE REFERENCE: MAL-UOUDCAN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR PLING DATE: 2003-02-16
PRIOR PLING DATE: 2003-02-16
PRIOR PLING DATE: 2000-02-17
PRIOR PLING DATE: 2000-03-16
PRIOR PLING DATE: 2000-05-25
PRIOR PLING DATE: 2000-06-17
PRIOR PLING DATE: 2000-09
PRIOR PLING DATE: 2000-07-18
PRIOR PLING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 6223-13
SOFTWARE: FASTSEQ FOR WINDOWS VERSION 4.0
SERNGTH: 1481
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LOCATION: 1, 2, 3, 4
OTHER INFORMATION: n = A,T,C or
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Matches 628; Conservative
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ORGANISM: Homo sapiens
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Sequence 21536, Application US/10357930

Publication No. US20040229086A1

GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Bndege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      678 GGGAACAATGGCTGAGCATATAACCATAGG---TATGGGAACAAAAAACATCAAAGTCAC
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Pred. No. 1.1e-185;
0; Mismatches 9;
                NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21476
LENGTH: 1481
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                                                                                                                                                    NAME/KEY: misc_feature; LOCATION: 1, 2, 3, 4; COTHER INFORMATION: n = A,T,C or US-10-357-930-21476
                                                                                                                                                                                                                                                          92.8%;
98.0%;
PRIOR FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 98.0°
Matches 628; Conservative
                                                                                               TYPE: DNA ORGANISM: Homo sapiens
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Sequence 21562. Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
TITLE OF INVENTION: IDENTIFICATION ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: IDENTIFICATION ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: IDENTIFICATION ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: UNMER: US/10/357,930
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
FRIOR APPLICATION NUMBER: 60/189,862
FRIOR FILING DATE: 2000-02-17
FRIOR PELICATION NUMBER: 60/189,862
FRIOR FILING DATE: 2000-02-17
FRIOR PELICATION NUMBER: 60/207,454
FRIOR FILING DATE: 2000-03-16
FRIOR FILING DATE: 2000-06-09
FRIOR FILING DATE: 2000-06-09
FRIOR FILING DATE: 2000-06-09
FRIOR FILING DATE: 2000-07-18
FRIOR APPLICATION NUMBER: 60/211,314
FRIOR APPLICATION NUMBER: 60/211,314
FRIOR APPLICATION NUMBER: 60/210,007
FRIOR FILING DATE: 2000-07-18
FRIOR FR
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Best Local Similarity 98.0%; Pred. No. 1.1e-185;
Matches 628; Conservative 0; Mismatches 9;
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ORGANISM: Homo sapiens
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Search completed: December 31, 2006, 13:56:01 Job time : 1032.23 secs

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9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*

11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11_NEW_PUB.seq:*
                                                                                                                                                                                              December 31, 2006, 12:26:03; Search time 222.451 Seconds (without alignments) 6266.684 Million cell updates/sec
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 308, App	Sequence 552, App		Sequence 221, App	Sequence 75529, A	Sequence 1766, Ap	Sequence 407591,	Sequence 478637,	Sequence 1, Appli	Sequence 214211,	Sequence 76796, A	Sequence 129607,	. Sequence 145, App	Sequence 46304, A	Sequence 35, Appl	Sequence 23957, A		Sequence 19300, A	Sequence 19357, A	Sequence 25041, A	Sequence 14, Appl	Sequence 609, App
SOUTHERES	ID	US-11-344-932-308	US-11-344-932-552	US-10-284-444-1570	US-11-174-307B-221	US-11-056-355B-75529	US-10-953-349-1766	US-11-266-748A-407591	US-11-266-748A-478637	US-11-454-296-1	US-11-266-748A-214211	US-11-266-748A-76796	US-11-266-748A-129607	US-11-330-726-145	US-11-056-355B-46304	US-11-454-296-35	US-11-266-748A-23957	US-11-266-748A-215548	US-10-449-902-19300	US-10-449-902-19357	US-10-449-902-25041	US-11-293-582-14	US-10-539-228-609
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de	Query Match	100.0	95.8	9.1	5.7	5.7	5.6	5.5	5.5	5.4	5.4	5.4	5.4	5.3	5.2	5.2	5.2	5.1	2.0	5.0	5.0	5.0	5.0
	Score	646	599.2	58.6	36.6	36.6	36	35.4	35.4	34.8	34.6	34.6	34.6	34.4	33.8	33.4	33.4	33	32.6	32.6	32.6	32.4	32.4
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Sequence 534, App	Sequence 1606, Ap	Sequence 10070, A	Sequence 75580, A	Sequence 1529, Ap	Sequence 1072, Ap	Sequence 29044, A	Sequence 100812,	Sequence 153623,	Sequence 9, Appli	Sequence 2477, Ap	Sequence 101312,	Sequence 112551,	Sequence 321, App	Sequence 37911, A	Sequence 25119, A	Sequence 22178, A	Sequence 39970, A	Sequence 214583,	Sequence 237140,	Sequence 18938, A	Sequence 121, App	Sequence 128, App	
US-10-540-898-534	US-11-073-360-1606	US-11-371-354-10070	US-11-371-354-75580	US-10-612-783-1529	US-11-218-305-1072	US-11-266-748A-29044	US-11-266-748A-100812	US-11-266-748A-153623	US-11-338-399-9	US-11-174-307B-2477	US-11-056-355B-101312	US-11-056-355B-112551	US-11-174-307B-321	US-11-056-355B-37911	US-10-449-902-25119	US-10-449-902-22178	US-11-266-748A-39970	US-11-266-748A-214583	US-11-266-748A-237140	US-10-449-902-18938	US-11-330-726-121	US-10-833-833-128	
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32.4	32.4	01	32.2	32.2	32.2	32.2	32	32	32	32	32	32	32	32	32	32	31.6		31.6	31.6	31.6	31.6	
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ALIGNMENTS

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RESULT.

19.5-108

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US-11-344-932-552
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APPLICANT:
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                                                                                                                                                                                              See File Wrapper
          FRIOR AFFLICATION NUMBER: 09/79,143
PRIOR FILING DATE: 2001-01-12
PRIOR AFLING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-09
PRIOR PILING DATE: 2000-10-10
PRIOR AFPLICATION NUMBER: 09/685,166
PRIOR FILING DATE: 2000-10-10
PRIOR FILING DATE: 2000-00-05
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: PASISEQ FOR WINDOWS Version 3.0
SEQ ID NO 308
APPLICATION NUMBER: 09/759,143
                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; LOCATION: 123
; OTHER INFORMATION: n = A,T,C or G
US-11-344-932-308
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 647; Conservative
                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: 106/14,678
PRIOR FILING DATE: 2002-05-09
PRIOR PELING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 09/852,911
PRIOR PLING DATE: 2001-05-09
PRIOR PLING DATE: 2001-05-09
PRIOR PLING DATE: 2001-05-09
PRIOR PLING DATE: 2001-01-02
PRIOR PLING DATE: 2001-01-12
PRIOR PLING DATE: 2001-01-12
PRIOR PLING DATE: 2000-11-09
PRIOR PLING DATE: 2000-10-00
PRIOR PLING DATE: 2000-11-09
PRIOR PLING DATE: 2000-10-00
PRIOR PLING DATE: 2000-10-00
PRIOR PLING DATE: 2000-10-00
PRIOR APPLICATION NUMBER: 09/651,279
PRIOR PLING DATE: 2000-00-06
PRIOR PRIOR PLING DATE: 2000-00-06
PRIOR PLING DATE: 2000-00-06
PRIOR PRIOR PLING DATE: 2000-00-06
PRIOR PLING DATE: 2000-00-06
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Houghton, Raymond L.
Vinals y de Bassols, Carlota
Application US/11344932
5. US20060269532A1
                                                                                                     APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Falos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Fools, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Davick
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Best Local Similarity 98.0
Matches 628; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li, Samuel X.
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Sequence 552, Applic
Publication No. US20
GENERAL INFORMATION:
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                      121 aagccricaaggracagarcrgaragcaa--aagagaaagggaacccraarcrcrrcrrgc 178
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TITLE OF INVENTION: UNCLECATIDE SEQUENCES AND POLYPEPTIDES ENCODED THER
TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERISTICS
TITLE OF INVENTION: USEFUL 50R MODIFYING PLANT CHARACTERISTICS
CURRENT APPLICATION NUMBER: US/11/174,307B
CURRENT FILING DATE: 2005-06-30
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,781
PRIOR PLING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,651
PRIOR FILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
PRIOR PILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 5544
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Pred. No. 0.31;
0; Mismatches 69;
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; LOCATION: (1)...(1566)
; OTHER INFORMATION: Also known as Ceres CDNA ID
US-11-17-307B-221
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US-11-056-355B-75529
US-11-056-355B-75529
Sequence 75529, Application US/11056355B
PUDLICATION NO. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA F)
TITLE OF INVENTION: Polypeptides Encoded Thei
TITLE OF TRERENCE: 2750-1590PUSC
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
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                                                                                                                                                                                                                                       Sequence 221, Application US/11174307B; Publication No. US20060143729A1; GENERAL INFORMATION: APPLICANT: ALEXANDROV, NICKOlai; APPLICANT: BROVER, Vyacheslav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/544,190
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OTHER INFORMATION: Ceres cDNA ID
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Best Local Similarity 53.1<sup>3</sup>
Matches 78, Conservative
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US-11-174-307B-221
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TGCTCAGGGGAAGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA
                                                                  CTAGAGAAAAGACCAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT
                                                                                                                                                                                                                                                                                                         CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT
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                                         421 GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAACAACATCAAAGTCAC
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Publication No. US20060188875A1

GENERAL INPORMATION:

APPLICANT: Cox, David

APPLICANT: Patil, Nila

APPLICANT: Hinds, David

TITLE OF INVENTION: Human Genomic Polymorphisms

FILE REFERENCE: 200/1013-11

CURRENT APPLICATION NUMBER: US/10/284,444

CURRENT FILING DATE: 2002-10-31

PRIOR PRICK FILING DATE: 2001-09-18
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64.8%; Pred. No. 4.5e-09;
tive 1; Mismatches 56;
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NUMBER OF SEQ ID NOS: 37858
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Best Local Similarity 64.8'
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Homo sapiens
US-10-284-444-1570
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US-10-284-444-1570
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                                                                                                                                                                                                                                                            460 ACAAAACAACATCAAAGTCACTGTATCAATTGCCATGAAGACTTGAGGACCTGAATCTA 519
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                                                                   Gaps
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APPLICANT: Applicant: Patrick
APPLICANT: Muligan, Karl
APPLICANT: Muligan, Karl
APPLICANT: Muligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR APPLICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105483.4
PRIOR APPLICATION NUMBER: EP 04105483.9
PRIOR PILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: US 60/662,276
PRIOR APPLICATION NUMBER: US 60/700,293
PRIOR PILING DATE: 2005-00-18
NUMBER: OF SEQ ID NOS: 483996
SOCTUMENT: 1750CTUMENT: 175
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DB 6; Length 1145;
   Score 36; DB 6; Length 114
Pred. No. 0.41;
0; Mismatches 105; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           580 TGGAAACAACAGAATGATTGCAAT 603
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      5.6%;
      Query Match
Best Local Similarity 48.55
Matches 99; Conservative
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US-11-266-748A-407591
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Best Local Similarity
Matches 51; Conserv
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US-11-266-748A-478637
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APPLICANT: ALEXANDROY, Nickclai et al.
TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONNED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VETSION 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)._[1566]
OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13503610
OTHER INFORMATION: as cited in SEQ ID NO 62416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1). (1566)
OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13657610
OTHER INFORMATION: as cited in SEQ ID NO 66165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1). T(1566)
OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13598312
OTHER INFORMATION: as cited in SEQ ID NO 68448
                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1). T(1566)
OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 15175923
OTHER INFORMATION: as cited in SEQ ID NO 54037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Ceres SEQ ID NO 13596100
in SEQ ID NO 68573
                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (1)._(1566)
OTHER INFORMATION: Ceres Seq. ID no. 6443376
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8.210-93-349-1766/c
; Sequence 1766, Application US/10953349
; Publication No. US20060107345A1
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; ORGANISM: Arabidopsis thaliana
US-10-953-349-1766
                                                                                                                                             TYPE: DNA
ORGANISM: Arabidopsis thaliana
          PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 75529
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OTHER INFORMATION: Ortholog
OTHER INFORMATION: as cited
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NAME/KEY: misc_feature
LOCATION: (1)..(1566)
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LOCATION: (1)..(1566)
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LENGTH: 1145
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                                                                                                                                                                                                                                                                                        72 AGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAAGGNGCCTCACA 131
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                                                                                                                           12 TATCATGTAAATCGGGTCACTCAAGGGGCCCAACCACAGCTGGGAGCCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ייי מוניסום Technology and Using the Same
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                                          73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50251 GCTTGGAGGGATATAAGATATAAGGAGACA 50221
                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 GTATAGATCTGGTAGCAAAGAAGAAGAACA 162
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APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray
TITLE OF INVENTION: Methods of Using the Sam
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
    Pred. No. 11;
0; Mismatches
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: EP 04105479.2
PRIOR FILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105482.6
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105507.0
PRIOR PLICATION NUMBER: EP 04105485.9
PRIOR APPLICATION NUMBER: EP 04105484.2
PRIOR PILING DATE: 2004-11-03
PRIOR PLING DATE: 2004-11-03
PRIOR PLING DATE: 2005-03-14
PRIOR PLING DATE: 2005-03-14
PRIOR PLING DATE: 2005-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 214211, Application US/11266748A Publication No. US20060134663A1 GENERAL INFORMATION:
APPLICANT: Harkin, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           c, g, or t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               537 GATACCTGACTCACTGT 521
Best Local Similarity 51.7%;
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PatentIn version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.3%;
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LOCATION: (865).

CTHER INFORMATION: n is a,

US-11-266-748A-214211
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Best Local Similarity 53.33
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-11-266-748A-214211/c
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SEQ ID NO 214211
LENGTH: 943
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Publication No. US20060286588A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: SAINZ, Jeeus

TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR

TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR

TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR

TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR

TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR

TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR

TILLE OF INVENTION: GENETIC VARIANTS IN GO/692,174

PRIOR APPLICATION NUMBER: US 60/692,174

PRIOR PILLING DATE: 2006-020

PRIOR FILLING DATE: 2006-01-06

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PATENTIN VERSION 3.3

SOFTWARE: PATENTIN VERSION 3.3

SOFTWARE: PATENTIN VERSION 3.3
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                                                                                                                                            APPLICANT: Harkin, Faul
APPLICANT: Harkin, Faul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REPERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: US/11/266,748A
CURRENT FILING DATE: 2005-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-01-14
PRIOR FILING DATE: 2005-01-14
PRIOR FILING DATE: 2005-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35.4; DB 8; Length 715;
Pred. No. 0.5;
0; Mismatches 26; Indels
Sequence 478637, Application US/11266748A Publication No. US20060134663A1
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SOFTWARE: PatentIn version 3
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Best Local Similarity 66.2<sup>†</sup>
Matches 51, Conservative
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US-11-266-748A-478637
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ORGANISM: Homo sapiens
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LENGTH: 715
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347 AGGGICAATITIGCICATITITIGIGIGIGAGAAAGICAGGATGCCCAGGGGCCCAGAGCAGG 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                407 GGGCTGCTTTGGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAAC 466
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US-11-330-726-145

US-11-330-726-145

Sequence 145, Application US/11330726

Publication No. US20060204982A1

GENERAL INFORMATION:

APPLICANT: Engelhard, Eric

APPLICANT: Engelhard, Exic

APPLICANT: Morris, David

TITLE OF INVERTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER

FILE REPERENCE: 2036-011002

CURRENT APPLICATION NUMBER: US/11/330,726

CURRENT APPLICATION NUMBER: US 10/052,482

PRIOR APPLICATION NUMBER: US 09/74,377

PRIOR APPLICATION NUMBER: US 09/74,377

PRIOR APPLICATION NUMBER: US 09/798,586

PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 241

SOFTWARE: PatentIn version 3.1 ...

LENGTH: 87977
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Pred. No. 1.1;
0; Mismatches 64; Indels
PRIOR FILING DATE: 2004-11-03
PRIOR PELICATION NUMBER: EP 04105507.0
PRIOR FILING DATE: 2004-11-03
PRIOR APPLICATION NUMBER: EP 04105485.9
PRIOR PILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2005-01-14
PRIOR FILING DATE: 2005-03-14
PRIOR FILING DATE: 2005-07-18
NUMBER OF SEQ ID NOS: 483996
SOFTWARE: PATENTIN VETSION 3.3
LENGTH: 945
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LOCATION: (8834)..(8882)
OTHER INFORMATION: n = a, c, g, or t
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Best Local Similarity 53.3%;
Matches 73; Conservative
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LOCATION: (2001)..(2048)
OTHER INFORMATION: n = a,
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LOCATION: (6720)..(7498)
OTHER INFORMATION: n = a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    347 AGGGTCAATTTGCTCATTTTGTGTGGATAAAGTCAGGATGCCCAGGGGCCAGAGCAGG
          US-11-266-748A-76796/C
US-11-266-748A-76796/C
US-11-266-748A-76796/C
US-11-266-748A-76796/C
US-11-266-748A-76796/C
Sequence 76796, Application US/11266748A
Fublication No. US20060134663A1
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICATION NUMBER: EP 0410549.2
FRIOR FILING DATE: 2004-11-03
FRIOR FILING DATE: 2005-07-18
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Publication No. US20060134663A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Harkin, Paul
APPLICANT: Mulligan, Karl
APPLICANT: Mulligan, Karl
TITLE OF INVENTION: Transcriptome Microarray Technology and
TITLE OF INVENTION: Methods of Using the Same
FILE REFERENCE: 55815-0102 (319189)
CURRENT APPLICANTON NUMBER: US/11-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-11-266-748A-76796
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US-11-266-748A-129607
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| Sequence 46304, Application US/11056355B |
| Sequence 46304, Application US/11056355B |
| Sequence 46304, Application No. US20060150283A1 |
| GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Brover, Vyacheslav |
| APPLICANT: Brover, Vyacheslav |
| TILLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding |
| TILLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding |
| TILLE OF INVENTION: Polypeptides Encoded Thereby |
| FILE REFERENCE: 2750-1590PUS2 |
| CURRENT APPLICATION NUMBER: 60/544,190 |
| PRIOR APPLICATION NUMBER: 60/544,190 |
| PRIOR FILING DATE: 2004-02-13 |
| NUMBER OF SEQ ID NOS: 119966 |
| SEQ ID NO 46304 |
| LENGTH: 2704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            463 AAACAACATCAAAGTCACTGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 TAMAGTCAGGATGCCCAGGGGCCAGGGGGGCTGCTTGCGTACAATGGCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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LOCATION: (1)...(2704)
OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13582297
OTHER INFORMATION: as cited in SEQ ID NO 56486
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NAME/KEY: misc_feature
LOCATION: (1)..(2704)
OTHER INFORMATION: Ortholog of Ceres SEQ ID NO 13586936
OTHER INFORMATION: as cited in SEQ ID NO 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
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Best Local Similarity 53.8%; Pred. No. 16;
Matches 71; Conservative 0; Mismatches
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| NAME/KEY: misc feature
| LOCATION: (45952)..(46750)
| OTHER INFORMATION: n = a, c, g, or t
| US-11-330-726-145
                                                                       NAME/KEY: misc_feature
LOCATION: (24443)..(24580)
OTHER INFORMATION: n = a, c, g, or t
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ORGANISM: Arabidopsis thaliana
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NAME/KEY: misc feature
(28778)..(28871)
OTHER INFORMATION: n = a, c,
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LOCATION: (16167)..(16186)
OTHER INFORMATION: n = a,
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LOCATION: (1)...(2704)
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Sequence 35, Application US/11454296

Publication No. US20060286588A1

GENERAL INFORMATION:

APPLICANT: GRAPT, SETUAN F. A.

APPLICANT: GRAPT, SETUAN F. A.

TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR TITLE OF INVENTION: GENETIC VARIANTS IN THE TCF7L2 GENE AS DIAGNOSTIC MARKERS FOR TITLE OF INVENTION NUMBER: US 60/692,174

PRIOR FILING DATE: 2005-06-20

PRIOR FILING DATE: 2006-01-06

PRIOR FILING DATE: 2006-01-06

NUMBER OF SEQ ID NOS: 53

SEQ ID NO 35

SEQ ID NO 35

FERMAN: APPLICATION VERSION 3:3
693 CTACACTCAAAAGCAACTTGACAACATCCAAGGAATTCACAGAAGCACCAGAAGCAGCGC 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 TATCATGTAAATCGGGTCACTCAAGGGGCCAACCACAGCTGGGAGCCACTGCTCAGGGGA 71
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Pred. No. 2.2;
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; ORGANISM: Homo sapiens
US-11-454-296-35
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Abv25790 Human pro
Abv25920 Human pro
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Aca59418 Human pro
Adgr6418 Human pro
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Abv11649 Human pro
Abv17499 Human pro
Abv27303 Human pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes isolated polypeptides, comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; prostate cancer; diagnosis; tumour; gene therapy; detection; immunogenic; cytostatic; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide useful for treating and diagnosing prostate cancer comprises an immunogenic portion of prostate tumor protein.
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ABV27364
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AAH93830
AAH93831
ACA59731
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ACC95458
ADB14002
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AAZ95017
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98US-00116134.
98US-00159812.
99US-00232149.
99US-00232880.
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23-SEP-1998;
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15-JAN-1999;
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Aah02721 Prostate
Aah84970 Human pro
Aaf86940 Human P71
Aca5957 Prostate
Ab195120 Human P71
Aca59284 Prostate
Ab13758 Human pro
Ad51484 Human pro
Ad51484 Human pro
Abv21571 Human pro
Abv21571 Human pro
Abv21573 Human pro
Abv21587 Human pro
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                  GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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diagnosis; vaccine,

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immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polymucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polymucleotides encoding them, antigen presenting cells which express the polypeptides, antibodies against the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or antibodies for passive immuno therapy. A portion of the modulate the expression of the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAAA6241 to AAA6691 and AAX82000 to AAX82020 represent sequences used in the exemplification of
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100.0%; Pred. No. 6.6e-200;
iive 0; Mismatches 0;
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Best Local Similarity 100.
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The present invention describes polymucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. (I) and (II) can be used or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastabis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent the present invention
                                                                                                                                                                                                                                                                                                                                     New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACCACCACGGTGGAGCCAC
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Retter MW, Stolk JA, Skeiky YAW;
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100.0%; Pred. No. 6.6e-200;
tive 0; Mismatches 0;
         prostate-specific;
              Human, prostate cancer, prostate-specific
cytostatic, gene therapy, metastasis, ss.
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Kalos MD, Fanger GR, Day CH,
                                                                                                                                                   16-JAN-2001; 2001WO-US001574.
                                                                                                                                                                                14-JAN-2000; 2000US-00483672
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Human prostate-specific cDNA sequence P712P.

(first entry)

04-OCT-2001

AAH93656;

AAH93656
ID AAH9
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AAH93656 standard; cDNA;

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           CATTITIGICIOTOGATAAAGICAGGATGCCCAGGGGCCCAGAGCAGGGGGCTGCTTTT
                                                  GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAACAACATCAAAGTCAC
                                                                                        TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCATCTTAAGGCAGCA
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                                                                            TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCATCATAAGGCAGCA
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GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAACAACATCAAAGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human prostate-specific polypeptides and polynucleotides useful diagnosis and treatment of cancer, especially prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       relates to isolated prostate-specific polynucleotides,
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Carter D;
                                                                                                                                                                                                                                                                                                                cancer; ss; cytostatic; immunostimulant; tumour.
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                                                                                                                                                                                                                                                                                           prostate cDNA sequence #301
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2000US-00605783.
2000US-00636215.
2000US-00651236.
2000US-00657279.
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2000US-00685166.
2000US-00709729.
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2000US-00568100.
2000US-00570737.
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                                                                                                                                                                                                                                                                       (first entry)
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09-MAY-2000;
12-MAY-2000;
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27-JUN-2000;
09-AUG-2000;
29-AUG-2000;
06-SEP-2000;
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protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The prostate specific polynucleotide of the invention
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                                                                                                                                              Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;
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prostate cancer; immunogenic; cytostatic; vaccine; ss.
                                                                                                                                                                                           100.0%; Score 646; DB 4; L
100.0%; Pred. No. 6.6e-200;
ive 0; Mismatches 0;
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nes 647; Conservative
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The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polymucleotides (N1) encoding (P1). (P1) and (N1) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P775P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Bye Syndrome region.

AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide and polypeptide sequences used in the exemplification of the present
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                   1 ACGATTTTCATTATCATGTAAAATCGGGTCACTCAAGGGGCCAACCACCACGGGGGAGGCCAC
GGACCAGTTTGAGTGGCAACAATGCAGCAGCAGAATCAATGGAAACAACAGAATGATTGC
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Wang A;
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                                                                                                                                                                                                                                                                                                                                            Human; prostate cancer; therapy; diagnosis; cat eye syndrome; chromosome 22q11.2; prostate-specific protein; chromosome 1; prostate specific antigen; PSA; ss.
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                                                                      Indels
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Skeiky YAW,
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100.0%; Pred. No. 6.6e-200;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                              Human prostate-specific cDNA sequence P712P.
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Kalos MD, Retter MW, Stolk JA,
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                                                                                                                                                                                                                                                                                                            The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have eytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression of a cancer, especially prostate cancer. AAH02422 to AAH2872, AAB7498 to AAB74810 are sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                        Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer.
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100.0%; Pred. No. 6.6e-200;
tive 0; Mismatches 0;
                                                                                                                                                    Cheever MA;
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                                                                                                                                                    Xu J, Skeiky YAW, Reed SG,
                                         04-OCT-2000; 2000WO-US027464
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The present invention describes compositions comprising peptides derived from the Wilm's tumour protein WT1 and methods for their use in treating malignant diseases. Peptides derived from both the murine and human WT1 proteins are provided. The human WT1 gene is found on chromosome 11p13, and the protein was shown to be a zinc finger transcription factor. The immunogenic peptides of the invention are particularly useful in the diagnosis and treatment of cancer and leukaemia. The present sequence is a coding sequence used in the exemplification of the invention
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Best Local Similarity 100.0%; Pred. No. 6.6e-200;
Matches 647; Conservative 0; Mismatches 0;
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13-JUL-1999;
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25-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence represents a prostate cancer therapy associated cDNN. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at sequence. Last of the printed specification, but was obtained in electronic format uspito.gov/sequence.html?DocID=US20020192763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer.
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prostatic acid phosphatase; PAP; prostate specific membrane antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kalos MD;
Carter D;
Hural J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; SEQ ID NO 308; 85pp; English.
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100.0%;
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28-MAR-2001; 2001US-00822827.
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Best Local Similarity 100.
Matches 647; Conservative
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Y DE BASSOLS C V.
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MITCHAM J L.
HARLOCKER S L.
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KALOS M D.
FANGER G R.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
WANG A.
SKEIKY Y A W.
HEPLER W T.
HENDERSON R A.
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                                PSMA; gene; ss
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The present invention relates to novel prostate-specific proteins (PSP) and their coding sequences. The PSPs and their coding sequences are useful for stimulating an immune response in a patient, or for treating prostate cancer in a patient and for determining, detecting or diagnosing the presence of a cancer in a patient. The present sequence was used to
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                                                                                                                                                                                                                                                                      CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT
                                                                               CATTITICEGEGGGGGATAAAGTCAGGATGCCCAGGGGCCAGAGGGGGCCAGAGGGGGCTTTT
                                                                                                                                                          GGGAACAATGGCTGAGCATAACCATAGGTTATGGGGAACAAAACAACATCAAAGTCAC
                                                                                                                                                                                                                     481 TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCATCTTAAGGCAGCA
                                                                                                                             GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAACAACATCAAAGTCAC
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                                                                                                                                                                                                                                                                                                                    647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytostatic, gene therapy, prostate-specific protein, PSP, immune response, prostate cancer; 88.
                                                                                                                                                                                                                                                                                                                                  AATGECCTTTTTTTCTCCTGCTTCTGACTTGATAAAGGGGGACCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prostate tumour specific cDNA sequence SEQ ID 308
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29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
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Mcneill PD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA described in the invention
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Carter D;
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100.0%; Pred. No. 6.6e-200;
ive 0; Mismatches 0;
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2000US-00483672.
2000US-00536857.
2000US-00570737.
2000US-00593793.
2000US-00605783.
2000US-0065783.
2000US-00651236.
2000US-00657279.
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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MITCHAM J L.
HARLOCKER S I
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RETTER M W.
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DAY C H.
                                                                                                                                                                                                                                                    JIANG Y.
KALOS M D.
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                             09-MAY-2000; 2
12-MAY-2000; 2
13-JUN-2000; 2
27-JUN-2000; 2
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29-AUG-2000; 2
06-SEP-2000; 2
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(KALO/)
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                                                                 1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCCAACCACAGGTGGGAGCCAC
                                                                          ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCCACCACCACCAGCTGGAGGCCAC
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               Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;
                                                Indels
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100.0%; Score 646; DB 8; L
Best Local Similarity 100.0%; Pred. No. 6.6e-200;
Matches 647; Conservative 0; Mismatches 0;
illustrate the invention
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Human; 88; prostate specific cDNA; cytostatic; immunostimulant; gene therapy; cell therapy; vaccine; T-cell epitope; class I major histocompatibility complex allele; MHC; prostate cancer; tumour; antigen presenting cell.
                                                                                 Human prostate specific cDNA P7112P.
          ADB13758 standard; cDNA; 647 BP
                                                        (first entry)
                                                                                                                                                                       sapiens.
                                                          18-DEC-2003
                                  ADB13758;
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ADB13758
          BXBXSXXXXXXXXXXXXXX
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02-OCT-2003

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New isolated polypeptide for use in a vaccine for stimulating an immune response, or for treating or diagnosis cancer, preferably prostate
                                                                       98US-00030607.
98US-00115453.
98US-00159812.
99US-00232149.
99US-00352616.
                                                                                                                                                                                 990S-00443686.
2000US-00483672.
2000US-0058572.
2000US-00570737.
2000US-0059793.
2000US-0059783.
2000US-00651236.
2000US-00651236.
2000US-00651236.
2000US-00679426.
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2000US-00679426.
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2002US-00294025
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09-FEB-2001;
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 12-NOV-2002;
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09-APR-1999;
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Example 3; Page; 101pp; English.

The invention relates to an isolated polypeptide comprising no more than 11-542 amino acids of ADB1353 comprising a sequence ADB14487. The peptides comprises a fragment ADB13563 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MHC) alleles. ADB13563 is a polypeptide encoded by a human prostate specific cond, one of 648 disclosed as new. Also included are nucleic acids encoding the proteins and peptides, expression vectors, a host cell transformed with the vector, an isolated antibody (or antigen binding transformed with the vector, an isolated antibody (or antigen binding transformed with the vector, an isolated antibody (or antigen binding contacting as a period of a cancer in a patient (comprising contacting a patient comparing the amount of polypeptide to a predetermined cutory appearing as ADB13558, detecting the amount of polypeptide to a predetermined cutory appearing the presence of cancer), a fusion protein comprising the presence of cancer), a fusion protein comprising the peptides or proteins, stimulating or expanding T cells specific for a tumour protein comprising colls that express composition comprising the peptides, or compounds, determining the presence of a cancer in a patient and treating prostate cancer in a patient with the peptides or antigen presenting cells that express concer in a patient with the peptides or antigen presenting cells that expressing them, is used to detect the presence of cancer in a patient comprising them), is used to detect the presence of cancer in a patient. The peptides or antigen presenting cells condens and encoding them), is used to detect the presence of cancer in a patient. The peptides, or an oligonucleotide contingen-presenting cells the peptides, or an oligonucle antigen-presenting cells the peptides, or a tumour protein and antigen-presented

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     mudlein acids, antidocter, tusting protecting, total properties or treat prostate cancer in a patient. The present sequence is one of the disclosed human prostate specific cDNAs. Note: Except where otherwise indicated, the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence.ogov/sequence.html?DocID=20030185830.
                                                                                                                                                                                                                        1 ACGATITICATIATCATGIAAATCGGGTCACTCAAGGGGCCAACCACAGCTGGGAGCCAC
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                                                                                                                                                                   Gaps
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 T cell populations
                                                                                                                                      Length 647;
                                                                                                            Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;
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Pred. No. 6.6e-200;
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 antibodies, fusion proteins,
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The invention relates to human prostate-specific polypeptides and the polymucleotides encoding them. The invention also relates to an isolated antibody or its antigen-binding fragment that specifically binds a polypeptide of the invention, a method of detecting cancer in a patient comprising contacting a biological sample of the patient with an agent that binds a prostate-specific polypeptide and comparing the amount of bound polypeptide compared to a predetermined cut-off value and a fusion protein comprising a prostate-specific polypeptide. The sequences of the invention are used to diagnose and treat cancer, particularly prostate cancer. This sequence represents cDNA encoding a human prostate-specific polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at sequence.html.
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JA, Day CH, Vedvick TS;
Henler WT, Hural J;
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Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH
Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT,
Mcneill PD, Houghton RL, Vinals Y De BassolsC, Fo
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09-MAY-2000; 2000US-00568100.

12-MAY-2000; 2000US-0057037.

13-JUN-2000; 2000US-00593793.

27-JUN-2000; 2000US-00593793.

09-AUG-2000; 2000US-00636215.
                                                                                                                        97US-00904804.
98US-0003056.
98US-00115453.
98US-00159812.
99US-00232149.
99US-00352616.
99US-0043586.
2000US-0043686.
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06-SEP-2000; 2000US-00657279.
02-OCT-2000; 2000US-00659426.
10-OCT-2000; 2000US-00685166.
09-NOV-2000; 2000US-00709729.
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09-FEB-2001; 2001US-00780669.
09-MAY-2001; 2001US-00852911.
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18-NOV-1999;
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Meagher MJ,
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23-SEP-1998
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1 ACGATITICATIATCATGIAAATCGGGTCACTCAAGGGGCCCAACCACGAGGTGGGAGCCAC 60

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GGACCAGTTTGAGTGGCAACAATGCAGCAGCAGAATCAATGGAAACAACAGAATGATTGC
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100.0%; Pred. No. 6.6e-200;
tive 0; Mismatches 0;
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Matches 647; Conservative
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14-JAN-2000; 2
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TGCTCAGGGGAAGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA
                                       CCACCCCTCTGACCCTTTTGGAACTCCTCTGACCCTTTAGAACAAGCCTACTAATATCTG
                                                                                                               CCACCCCTCTGACCCTTTGGAACTCCTCTGGACTCCTTTAGAACAAGCCTAATATCTG
                                                                                                                                        CTAGAGAGAAGACCACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT
                                                                                                                                                  CTTGGCTAAGATGTGGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT
                                                                                                                                                                                             CTIGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT
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                                                                                                                                                                                                                                   GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAACAACATCAAAGTCAC
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97US-00904804.
98US-00020956.
98US-00115453.
98US-00159112.
99US-00232149.
99US-00332616.
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01-AUG-1997;
09-FEB-1998;
25-FEB-1998;
14-JUL-1998;
23-SEP-1998;
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09-APR-1999;
13-JUL-1999;
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fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New fusion protein comprising a P501S polypeptide and an unrelated fu partner, useful for diagnosing, preventing, or treating cancer, such prostate cancer.
                                                                                                                                                                                                                                                                                                  Y, Reed SG;
Vedvick TS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 647 BP; 190 A; 141 C; 154 G; 161 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                  Jiang Y
Day CH,
                                                                                                                                                                                                                                                                                              Xu J, Dillon DC, Mitcham JL, Harlocker SL,
Kalos MD, Fanger GR, Retter MW, Stolk JA,
Carter D, Li SX, Wang A, Skeiky YAW;
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99US-00439313.
99US-00443686.
2000US-00483672.
2000US-00536857.
2000US-00568100.
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541 GGACCAGTTTGAGTGGCAACAATGCAGCAGCAGAATCAATGGAAACAACAAGAATGATTGC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated polypeptide comprising no more than
                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide for use in a vaccine for stimulating an immune for treating or diagnosis cancer, preferably prostate
                                                                                                          Human; 88; prostate specific cDNA; cytostatic; immunostimulant; gene therapy; cell therapy; vaccine; T-cell epitope; class I major histocompatibility complex allele; MHC; prostate cancer; tumour; antigen presenting cell.
                                                                                                Human prostate antigen P712P additional DNA sequence.
                                                         ADB14484 standard; cDNA; 2577 BP
                                                                                                                                                                                                  97US-00806099.
97US-00904804.
98US-00020607.
98US-00115453.
98US-00159812.
99US-00232149.
99US-00232149.
99US-0043313.
99US-0043586.
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2000US-00593793.
2000US-00605783.
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                                                                                                                                                            US2003185830-A1.
                                                                                                                                               Homo sapiens
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09-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated
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Treell epitopes for 3 class I major histocompatibility complex (MIC)

Treell epitopes for 3 class I major histocompatibility complex (MIC)

Treell epitopes for 3 class I major histocompatibility complex (MIC)

alleles. ADB1363 is a polypeptide encoded by a human prostate specific

cond, one of 648 disclosed as may. Also included are nucleic acids

conding the proteins and peptides, expression vectors, a host cell

cransformed with the vector, an isolated antibody (or antigen binding

cransformed with the vector, an isolated antibody (or antigen binding

crample with a petifically binds to the protein or peptide, detecting

the presence of a cancer in a patient (comprising contracting a patient

cample with a binding agent that binds to the peptides or a polypeptide

comprising the peptides or proteins to polypeptide that binds to

comprising the peptides or proteins stimulating or expanding T cells

septides or the isolated T cell population, treating prostate cancer in

comprising the peptides or proteins stimulating or expanding T cells

specific for a tumour protein comprising contacting T cells with the

comprising the peptides or compounds, determining the presence of

cancer in a patient and treating a composition comprising the peptides or that the Peptides or antigen presence of the peptides or antigen presence of an election comprising the

concer in a patient with the peptides or antigen presenting calls that express

cracer in a patient with the peptides or antigen presenting calls and election comprised or antigen. The peptides or antigen present of differentiation (CD4+) and/or CD8+ T cells isolated

from a patient with the peptides or antigen presenting calls antigen. The peptides, are used to cancer in a patient. The peptides, or an oligonucleoride

cracer in a patient and are used to estimulate or expand T cells specific for a tumour protein. The peptides, are used to simulate or expand T cells specific for a tumour protein. The peptides, secundate cancer in a patient. The present sequence is a 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGAACAATGGCTGAGCATATAACCATAGG---TATGGGAACAAAAACATCAAAGTCAC 1111
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Pred. No. 8e-185;
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Best Local Similarity
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1 ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCAACCACAGCTGGGAGCCAC
                                                  TGCTCAGGGGAAGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA
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2000US-0189862P.
2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
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25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
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                                                                                          GGACCAGTTTGAGTGGCAACAATGCAGCAGCAGAATCAATGGAAACAACAGAATGATTGC 1231
                                                                                                                                                                                                                                                                                                                 Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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Best Local Similarity 98.0%; Pred. No. 2e-184;
Matches 628; Conservative 0; Mismatches 9
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Monahan JE Endege WO, Schlegel R,

WPI; 2001-662795/76

Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.

Claim 1; Page 3587; 11750pp; English

The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate calc in in a patient; (f) assessing the prostate cancer in a patient; determining whether prostate cancer has metastasized in a patient; (d) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker

Sequence 1481 BP; 364 A; 346 C; 314 G; 453 T; 0 U; 4 Other;

Gaps 4 ; Length 1481; Indels Score 599.2; DB 5; Pred. No. 2e-184; 0; Mismatches 9; Query Match 92.8%; Best Local Similarity 98.0%; Matches 628; Conservative

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Homo sapi
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PC CIZNIS/09, A61K38/00, A61K39/00, A61K39/395, C07K14/47, C07K16/30,
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1 (bases 1 to 647)

Dillon, D.C., Harlocker, S.L., Yuqiu, J., Xu, J. and Mitcham, J.L.

Compounds for immunotherapy and diagnosis of prostate cancer and
methods for their use

Patent: JP 2002520054-A 300 09-JUL-2002;

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Location/Qualifiers (11. 647).
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E 1 (bases 1 to 647)

(S Xu,J., Dillon,D.C. and Mitcham,J.L.
Compounds for immunotherapy of prostate can their use

NAL Patent: US 6465611-A 308 15-OCT-2002;
Corixa Corporation; Seattle, WA Location/Qualifiers

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                                         100.0%; Score 646; DB 2; L
larity 100.0%; Pred. No. 7.6e-202;
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of prostate
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L. and Yuqiu,J. Prostate specific fusion protein compositions
Patent: US 6395278-A 308 28-MAY-2002;
Corixa Corporation; Seattle, WA
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    /organism="unknown"
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tive 0;
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Sequence 308 from patent
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Best Local Similarity 100.
Matches 647; Conservative
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yuqiu,J.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and
Day,C.H.
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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Query Match
Best Local Similarity 100.0%;
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                    Gaps
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1 (bases 1 to 647)

1 (bases 1 to 647)

Kalos,M.D., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.
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100.0%; Pred. No. 7.6e-202;
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/organism="unknown"
/mol_type="genomic DNA"
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Sequence 308 from patent
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of prostate
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Corixa Corporation; Seattle,
WOX;
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skelky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA"
/mol_type="genomic DNA"
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of prostate
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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/organism="unknown"
/mol_type="genomic DNA'
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Xalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of prostate
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Corixa Corporation; Seattle, WA
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   /mol_type="genomic DNA
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                                     /mol_type="genomic
                          /organism="unknown"
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,

Xalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,

Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,

Hepler,W.T. and Henderson,R.A.

Compositions and methods for the therapy and diagnosis of pi
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Patent: US 6894146-A 308 17-MAY-2005;
Corixa Corporation; Seattle, WA
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            /organism="unknown"
/mol_type="genomic
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AR656944
AR656944.1 GI:67590056
                                                           Query Match
Best Local Similarity 100.0%;
Matches 647; Conservative 0
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07-0CT-2005 Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Xu,J., Dillon,D.C., Mitcham,J.L., Warlot,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T., Henderson,R.A., Hural,J., MoNeill,P.D., Houghton,R.L.,
Vinals y de Bassols,C., Foy,T.M., Watanabe,Y. and Meagher,M.J.
Compositions and methods for the therapy and diagnosis of prostate 420 120 120 180 180 240 240 CTAGAGAAAAGACCAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300 300 360 360 420 480 480 540 540 909 9 9 acgartritcarrarcargraaarceegrcacrcaaegeeccaaccacaegereega TGCTCAGGGGAAGGTTCATATGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA GGNGCCTCACAGTATAGATCTGGTAGCAAAGAAGAAGAACAAAAAACACTGATCTTTTCTG CTAGAGAAAAGACCAAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT CATITITICITGIGGATAAAGTCAGGATGCCCAGGGGCCAGAGCAGGGGCTGCTTGTTT GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAACAACATCAAAGTCAC TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTAACCGATTCATCTTAAGGCAGCA rerarcaarreccargaagacrrgagggaccrgaarcraccgarrcarcrraaggcagga GGACCAGTTTGAGTGGCAACAATGCAGCAGCAGAATCAATGGAAACAACAGAATGATTGC <u> ACGATTTTCATTATCATGTAAATCGGGTCACTCAAGGGGCCCAACCACAGCTGGGAGCCAC</u> Gaps PAT ; 0 647 647 Indels AATGTCCTTTTTTTTCTCCTGCTTCTGACTTGATAAAAGGGGACCGT

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RESULT 14 AX106197 LOCUS REFERENCE AUTHORS TITLE JOURNAL

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Primates; Catarrhini;
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                                                                                                                                           100.0%; Score 646; DB 2; L
llarity 100.0%; Pred. No. 7.6e-202;
Conservative 0; Mismatches 0;
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Mammalia, Eutheria, Euarchontoglires, Pr
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WO0125272.
CORIXA CORPORATION (US)
Location/Qualifiers
1. .647
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/ mol_type="unassigned DNA"
/ db xref="taxon:9606"
/ feature
1. .647
/ note="n = A,T,C or G"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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   Patent: US 6943236-A 308 13-SEP-2005;
Corixa Corporation; Seattle, WA
Location/Qualifiers
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                                                                         /mol_type="genomic DNA
                                           1. .647
/organism="unknown"
                                                                                                                   100.0%;
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/note="n = A,T,C or G"
               cancer
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i Sequence 308, Application US/09439313

patent No. 6329505

i GENERAL INFORMATION:

i APPLICANT: Xu, Jiangchun

i APPLICANT: Mitcham, Jennifer L.

APPLICANT: Hitcham, Jennifer L.

APPLICANT: Reed, Steven G.

APPLICANT: Reed, Steven G.

APPLICANT: Reter, Mark

APPLICANT: Retter, Mark

APPLICANT: Retter, Mark

APPLICANT: Retter, Mark

APPLICANT: Retter, Mark

APPLICANT: OBY, CohyoSITIONS AND METHODS FOR THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210.1.427C9

CURRENT APPLICATION NUMBER: US/09/439,313

CURRENT FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 575

SOFTWARE: FREESE SEG FO: Windows Version 3.0

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US-09-949-002-167

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100.0%; Pred. No. 2.1e-206;
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US-09-651-236-552
US-09-657-279-552
US-10-012-896-552
US-10-144-678A-552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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APPLICANT: Xu, Jiangchun
BAPLICANT: AL, Jiangchun
APPLICANT: Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.4276
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastERQ for Windows Version 3.0
FEATURE OF SEQ ID NOS: 338
SOFTWARE: PASTER OF WINDOWS SEQ ID NOS: 308
FEATURE OF SEQ ID NOS: 308
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100.0%; Pred. No. 2.1e-206;
Live 0; Mismatches 0;
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8.09-232-149A-308
; Sequence 308, Application US/09232149A
; Patent No. 6465611
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; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-308
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Best Local Similarity 100.0
Matches 647; Conservative
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NAME/KEY: misc_feature
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APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: OCPOROUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C8
CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT APPLICATION NUMBER: US/09/352,616A
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 308
LENGTH: 647
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Sequence 308, Application US/09352616A
Sequence 308, Application US/09352616A
Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
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OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapien
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100.0%; Pred. No. 2.1e-206;
iive 0; Mismatches 0;
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US-09-685-166A-308
; Sequence 308, Application US/09685166A
; Patent No. 6630305
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APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Rolk, John A.
APPLICANT: Boy, Craig H.
APPLICANT: Craig H.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Davick, Thomas S.
                                                                   = A,T,C or
                                                                                                                                Query Match
Best Local Similarity 100.
Matches 647; Conservative
                        NAME/KEY: misc feature;
LOCATION: (1)...(647)
CTHER INFORMATION: n = US-09-636-215-308
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APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFRENCE: 2010.21.42717C17

CURRENT APPLICATION NUMBER: US/09/636,215

CURRENT FILING DATE: 2000-08-10

NUMBER OF SEQ ID NOS: 852

SOFTWARE: FastSEQ for Window-

LENGTH: 647

TYPE: PASSIVE AND METHORS AND METHODS FOR THE THERAPY AND

TYPE: PASSIVE AND METHORS AND METHORS AND METHODS FOR THE THERAPY AND

TYPE: PASSIVE AND METHORS AND METHORS
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Patent No. 6620922
GENERAL INFORMATION:
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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ORGANISM: Homo sapien
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US-09-636-215-308
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NAME/KEY: misc_feature

: LOCATION: (1)...(647)

: OTHER INFORMATION: n = A.T.C or

US-09-688-489-308
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Best Local Similarity 100.
Matches 647; Conservative
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APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.427021
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 308
LENGTH: 647
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LOCATION: (1)...(647)
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Homo sapien
FEATURE:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: M. Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CONCOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CONCOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CONCOUNDS FOR IMMUNOTHERAPY OF PROSTATE
CURRENT APPLICATION NUMBER: US/09/688,489
CURRENT FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FASESEQ FOR Windows Version 3.0
LENGTH: 647
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RESULT 7 US-09-679-426-308

RESULT 6 US-09-688-489-308 ; Sequence 308, Application US/09688489

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Samuel
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US-09-759-143-308
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                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER TITLE REPERENCE: 210121.427C20
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
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100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.16-206;
Matches 647; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                        FastSEQ for Windows Version 3.0
Application US/09679426
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (1)...(647)
OTHER INFORMATION: n = A,T,C or G
                                      Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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Wang, Aijun
Skeiky, Yasir A.W.
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Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas
Carter, Darrick
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ORGANISM: Homo sapien
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LENGTH: 647
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE SEPERENCE: 210121.427023
CURRENT APPLICATION VUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
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100.0%; Pred. No. 2.1e-206;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                       Sequence 308, Application US/09759143
Patent No. 6800746
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; OTHER INFORMATION: n = A,T,C or G
US-09-759-143-308
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Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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Vedvick, Thomas S.
Carter, Darrick
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Dillon, Davin C.
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Retter, Marc W.
Stolk, John A.
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Best Local Similarity 100.
Matches 647; Conservative
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SOFTWARE: FastSEQ for
SEQ ID NO 308
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ORGANISM: Homo sapien
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APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, John A.
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Vedvick, Thomas S.
Carter, Darrick
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US-09-657-279-308
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                                                   CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT
                                                                                                                CATTTTGTGTGGATAAAGTCAGGATGCCCAGGGGCCAGAGGGGGGGCTGCTTTT
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APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210.21.42718C18
CURRENT APPLICATION NUMBER: US/09/651,236
CURRENT APPLICATION NUMBER: US/09/651,236
NUMBER OF SEQ ID NOS: 865
SOFTWARE: FastSEQ for Windows Version 3.0
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100.0%; Score 646; DB 3; Length 647;
Best Local Similarity 100.0%; Pred. No. 2.1e-206;
Matches 647; Conservative 0; Mismatches 0; Indels
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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NAME/KEY: misc_feature
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ORGANISM: Homo sapien
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US-09-651-236-308
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APPLICANT: Xu, Jian
APPLICANT: Dillon,
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US-09-651-236-308
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LENGTH: 647
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GGGAACAATGGCTGAGCATATAACCATAGGTTATGGGGAACAAAACAACATCAAAGTCAC 480 CTAGAGAAAAGGCCAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300 361 CATTITGIGIGIGATAAAGICAGGAIGCCCAGGGGCCAGAGCAGGGGCTGCTIGCTIT 420 TGCTCAGGGGAAGGTTCATAGGGACTTTCTACTGCCCAAGGTTCTATACAGGATATAAA 120 CTAGAGAAAAGACCAACAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT TGTATCAATTGCCATGAAGACTTGAGGGACCTGAATCTACCGATTCATCTTAAGGCAGCA GGACCAGTITGAGTGGCAACAATGCAGCAGCAGAATCAATGGAAACAACAAATGATTGC CATTTGTGTGTGGATAAGTCAGGATGCCCAGGGGCCCAGAGCAGGGGGCTGCTTTGCTTT APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121-427C19
CURRENT APPLICATION NUMBER: US/09/657,279
CURRENT FILING DATE: 2000-09-06
NUMBER OF SEQ ID NOS: 877
SOFTWARE: FastSEQ for Windows Version 3.0 647 647 601 AATGTCCTTTTTTTTCTCCTGCTTCTGACTTGATAAAAGGGGACCGT AATGTCCTTTTTTTTTTCTCCTGCTTCTGACTTGATAAAAGGGGACCGT

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                                                                                                                                                           APPLICANT: Foy, Teresa APPLICANT: Fanger, Gary R. APPLICANT: Fanger, Gary R. APPLICANT: Wantanbe, Yoshihiro APPLICANT: Wantanbe, Yoshihiro APPLICANT: Wantanbe, Yoshihiro APPLICANT: Wantanbe, Madeleine Joy TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY ITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FRSELSEQ for Windows Version 3.0
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100.0%; Pred. No. 2.1e-206;
tive 0; Mismatches 0;
                                                                                       Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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                                Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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Best Local Similarity 100.
Matches 647; Conservative
                    Wang, Aijun
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ORGANISM: Homo sapiens
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                                                                                                                                           100.0%; Score 646; DB 3; L. Llarity 100.0%; Pred. No. 2.1e-206; Conservative 0; Mismatches 0;
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Patent No. 6943236
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
                                                                       ; LOCATION: (1)....(647)
; OTHER INFORMATION: n = A,T,C or US-09-657-279-308
                                                    NAME/KEY: misc_feature
LOCATION: (1)...(647)
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
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Best Local Similarity
Matches 647; Conserv
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                                                                      CTTGGCTAAGATGTGGGTTCCACATTAGGTTCTGAATATGGGGGGAAGGGTCAATTTGCT
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APPLICANT: Wang, Aijun.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.42777C17
CURRENT PILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOUTHARE: FastSEQ for Windows Version 3.0
ILENGTH: 2577
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Pred. No. 2.6e-190;
0; Mismatches 9;
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Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Dillon, Davin C.
Mitcham, Jennifer L.
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Matches 628; Conservative
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US-09-636-215-552
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APPLICANT: Hepler, William T.
APPLICANT: Hural, John
APPLICANT: Horbiton, Particia D.
APPLICANT: Howelton, Raymond L.
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Vinals y de Bassols, Carlota
APPLICANT: Foy, Teresa M.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427028
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 308
LENGTH 847
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                                                         601 AATGTCCTTTTTTTTTTCCTGCTTCTGACTTGATAAAGGGGACCGT 647
                                                                                                                                 RESULT 12
2.10-14-4678A-308
: Sequence 308, Application US/10144678A
; Patent No. 7033827
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NAME/KEY: misc_feature
LOCATION: 123
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                            J. PATENT NO. 7033827.

GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Henderson, Robert A.

APPLICANT: Fanger, Marchael D.

APPLICANT: Fanger, Gary R.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Obay, Craig H.

APPLICANT: Carter, Darrick

APPLICANT: Carter, Darrick
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Hepler, William T.
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Matches 647; Conservative
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ORGANISM: Homo sapiens
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Wang, Aijun
Skeiky, Yasir A.
Hepler, William
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Best Local Similarity
Matches 628; Conser
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  US-09-685-166A-552
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CTAGAGAAAAGACCAACGGCCTCAAAGGATCTCTTACCATGAAGGTCTCAGCTAATT 300
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                                    APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Sekiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: OOMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT APPLING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
                                                                                                                                                                                                                                                                                                                                                                                                                                         601 AATGICCTTTTTTTCTCCTGCTTCAAAAAGGG 641
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H. S.
Vedvick, Thomas S.
Carter, Darrick
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LENGTH: 2577
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                                    Gaps
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     Length 2577;
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Score 599.2; DB 3;
Pred. No. 2.6e-190;
0; Mismatches 9;
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
 92.8%;
98.0%;
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Vedvick, Thomas S
Carter, Darrick
Li, Samuel
                                    Conservative
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427720
CURRENT APPLICATION NUMBER: US/09/679,426
CURRENT FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 895
SOFTWARE: FASTSEQ FOR Windows Version 3.0
LENGTH: 2577
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                                                                                                                                                                                               Query Match 92.8%; Score 599.2; DB 3; Best Local Similarity 98.0%; Pred. No. 2.6e-190; Matches 628; Conservative 0; Mismatches 9;
                                                                                                                                      TYPE: DNA
CORGANISM: Homo sapiens
US-09-679-426-552
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completed: December 31, 2006, 12:31:09 ne : 153.014 secs Search cor Job time

Sequence 474, App Sequence 474, App Sequence 474, App Sequence 174, App Sequence 16001, A Sequence 12033, A Sequence 26, Appl

Sequence Sequence Sequence

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Sequence Sequence Sequence 1, Appli Sequence 1, Appli Sequence 13210, A

US-08-916-421B-1 US-09-692-570-1

ALIGNMENTS

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US-09-439-313-311

US-09-439-313-311

Sequence 311, Application US/09439313

Patent No. 6329505

GENERAL INFORMATION:

APPLICANT: Ni Jangchun

APPLICANT: Mitcham, Janinger L.

APPLICANT: Matcham, Janinger L.

APPLICANT: Matcham, Janing Yuqui

APPLICANT: Ranger, Gary

APPLICANT: Ranger, Gary

APPLICANT: Ranger, Gary

APPLICANT: Ranger, Gary

APPLICANT: Rols, Michael

APPLICANT: Rols, Michael

APPLICANT: Ranger, Gary

APPLICANT: Rols, John

TITLE OF INVENTION: DAY, Craig

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REPERENCE: 210121.427C9

CURRENT APPLICATION NUMBER: US/09/439,313

CURRENT FILING DATE: 1999-11-12

NUMBER OF SEQ ID NOS: 575

SEQ ID NO 311

EMERCH: 526

TUBICANT: SA
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100.0%; Pred. No. 9.5e-125;
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US-09-679-143-475
US-09-651-236-475
US-09-651-236-475
US-10-012-896-475
US-10-144-678A-475
US-09-439-13-474
US-09-685-166A-474
US-09-685-166A-474
US-09-651-236-474
US-09-651-236-474
US-09-651-236-474
US-10-144-678A-474
US-10-144-678A-474
US-10-144-678A-474
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OTHER INFORMATION: n = A,T,C or G
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   NAME/KEY: misc_feature
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ORGANISM: Homo sapien
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Best Local Similarity
Matches 526; Conserv
  US-09-439-313-311
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                                                                            December 31, 2006, 12:18:37 ; Search time 122.772 Seconds
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/BMC_celerra_SinS3/ptodata/2/ina/6_COMB.seq:*
/BMC_Celerra_SinS3/ptodata/2/ina/7_COMB.seq:*
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/BMC_celerra_SinS3/ptodata/2/ina/7_COMB.seq:*
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US-10-012-896-311
US-10-144-678A-311
US-09-439-313-476
US-09-636-215-476
US-09-636-16A-476
US-09-679-426-476
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Sequence 311, Application US/09232149A

Patent No. 646511

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
ITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
ITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A

CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338

SOFTWARE PRESERVE FASTERO FOR Windows Version 3.0
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LOCATION: (1)...(526)

OTHER INFORMATION: n = A,T,C or G

US-09-232-149A-311
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Matches 526; Conservative 0
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ORGANISM: Homo sapien
FEATURE:
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; Patent No. 6395278
; GENERAL INPORMATION:
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: W. Jiangy Yuqui
APPLICANT: W. Jiangchun
APPLICANT: W. Jiangchun
TITLE OF INVENTION: OP PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REPERRORE: 210121.42708
CURRENT APPLICATION NUMBER: US/999-07-13
CURRENT FILING DATE: 1999-07-13
NUMBER OF SEQ ID NOS: 472
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 311
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NAME/KEY: misc_feature
LOCATION: (1)...(526)
OTHER INFORMATION: n = A,T,C or
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ORGANISM: Homo sapien
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Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0;
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ITITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 111, Application US/09685166A Patent No. 6630305
GENERAL INFORMATION:
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| LOCATION: (1)...(526)
| OTHER INFORMATION: n = A,T,C or G
US-09-685-166A-311
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Henderson, Robert A.
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Fanger, Gary R.
Retter, Marc W.
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Vedvick, Thomas
Carter, Darrick
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US-09-685-166A-311
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CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
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Patent No. 6620922
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; OTHER INFORMATION: n = A,T,C or G
US-09-636-215-311
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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Skeiky, Yasir A.W.
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Vedvick, Thomas S
Carter, Darrick
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Retter, Marc W.
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US-09-636-215-311
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LENGTH: 526
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GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Robert A.
APPLICANT: Handerson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Darrick
APPLICANT: Day, Craig H.
APPLICANT: Li, Samuel
APPLICANT: Wasnel
APPLICANT: Hepler, William
APPLICANT: Wasnel
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Best Local Similarity 100.0%; Score 525; DB 3; L
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 311, Application US/09679426
Fatent No. 6759515
GENERAL INFORMATION:
APPLICANT: Xu, Jangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Retter, Machael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Michael D.
APPLICANT: Ralos, Stolk, John A.
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OTHER INFORMATION: n = A,T,C or G
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                                                             CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TATLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121-42702
CURRENT APPLICATION NUMBER: US/09/688,489
CURRENT FILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
IENGTH: 526
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US-09-688-489-311
Sequence 311, Application US/09688489
Patent No. 6664377
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| LOCATION: (1)...(526)
| OTHER INFORMATION: n = A,T,C or G
US-09-688-489-311
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Matches 526; Conserv
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                                                                                                              CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTTAGCTACAGGGGAAGCTAAATAA 180
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                                                                                   TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATTATATTATCTA
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  1 CABATTTGAGCCAATGACATAGAATTTTACAAAATCAAGAAGCTTATTCTGGGGCCCATTTC
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42718C18
FULE REFERENCE: 210121.42718C18
CURRENT APPLICANTION NUMBER: US/09/651,236
CURRENT APPLICANTION NUMBER: US/09/651,236
KUNBER OF SEQ ID NOS: 865
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6818751
GENERAL INFORMATION:
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Dillon, Davin C.
Mitcham, Jennifer L.
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Vedvick, Thomas
Carter, Darrick
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ORGANISM: Homo sapien
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                                CATITACAGCATITAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
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100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: n = A,T,C or G
US-09-759-143-311
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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ORGANISM: Homo sapien
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; SEQ ID NO 311
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE: in section: (1)...(526)
; COCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or G
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US-10-012-896-311
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                                                                         Gaps
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; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C19
; CURRENT APPLICATION NUMBER: US/09/657,279
; CURRENT FILING DATE: 2000-09-06
; NUMBER OF SEQ ID NOS: 877
; SOPTWARE: FARTCEN
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                                              Length 526;
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ive 0; Mismatches 0;
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Patent No. 6894146
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
     = A,T,C or
                                                           Best Local Similarity 100.
Matches 526; Conservative
       OTHER INFORMATION: n
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US-09-657-279-311
        ; OTHER INFORMA
US-09-651-236-311
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100.0%; Score 525; DB 3; L
Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0;
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Patent No. 6943236
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Alang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Carier, Darick
APPLICANT: Vedvick, Thomas S.
APPLICANT: Garter, Darrick
APPLICANT: Garter, Darrick
APPLICANT: Hepler, Milliam T.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
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Vinals y de Bassols,
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Watanabe, Yoshihiro
  Harlocker, Susan L.
                                                                                                                                                                                                                                                             Skejky, Yasir A. W.
Hepler, William T.
                      Jiang, Yuqiu
Henderson, Robert
Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                       Houghton, Raymond
                                                                                 Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
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Best Local Similarity 100.
Matches 526; Conservative
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ORGANISM: Homo sapiens
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                                                                                 APPLICANT: Fanger, Gary R.
APPLICANT: Wanteranabe, Yoshihiro
APPLICANT: Wanteranabe, Yoshihiro
APPLICANT: Wanteranabe, Yoshihiro
APPLICANT: Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT EPFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012,896
NUMBER OF SEQ ID MOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 100.0%; Pred. No. 9.5e-125;
Matches 526; Conservative 0; Mismatches 0;
                    Houghton, Raymond L.
Vinals de Bassols, Carlota
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; Sequence 311, Application US/10144678A
; Patent No. 7033827
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 499 OTHER INFORMATION: n = A,T,C or G
McNeill, Patricia D.
                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                      SEQ ID NO 311
LENGTH: 526
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APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE FEBERCE: 210121.427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT FILING DATE: 2002-08-12
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100.0%; Pred. No. 9.5e-125;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 311
LENGTH: 526
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; GENERAL INFORMATION:
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                                                                                                                                                    APPLICANT: Xu, Jiangchun
APPLICANT: Davin C.
APPLICANT: Mitcham, Davin C.
APPLICANT: Mitcham, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Ralos, Michael
APPLICANT: Ralos, Michael
APPLICANT: Ranger, Gary
APPLICANT: Renger, Gary
APPLICANT: Role, Michael
APPLICANT: Role, John Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3434;
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             481 AGTTCTATAAACTGTAGTNTACTTATTTTAATCCCCAAAGCACAGT
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Pred. No. 2.9e-110;
0; Mismatches 8;
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CURRENT FILING DATE: 1959-11-12
NUMBER OF DID NOS: 575
SOFTWARE: PARKEG FOR WINDOWS Version 3.0
                                                                                                       Sequence 476, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 97.9%;
Matches 507; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                            RESULT 13
US-09-439-313-476/c
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LENGTH: 3434
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3062 CAAATTTGAGCCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: LANGUAGES OF PROSTATE CANCER
FILE REPERENCE: 21012.42717C17
CURRENT PELING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
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2584 AGTICTATAAACTGTAGT-TACTTATTTTAATCCCAAA 2548
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                                                                                                                  , Sequence 476, Application US/09636215; Patent No. 6620922
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Matches 507; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: Li, Samuel
APPLICANT: Wing, Aijun
APPLICANT: Warst A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C21
CURRENT APPLICATION NUMBER: US/09/685,166A
CURRENT FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 898
SOFTWARE: FastSEQ for Windows Version 3.0
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                        481 AGTICTATAAACTGTAGINTACTIATITTAATCCCCAA 518
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                                                                                                                                                            Sequence 476, Application US/09685166A
Patent No. 6630305
GENERAL INFORMATION:
                                                                                                                                                                                                                           APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Jane A.
APPLICANT: Carter, Jennas S.
APPLICANT: Carter, Darrick
APPLICANT: Garet, Darrick
APPLICANT: Garet, Darrick
APPLICANT: Garet, Darrick
APPLICANT: Stelky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo sapiens
US-09-685-166A-476
                                                                                                                RESULT 15
US-09-685-166A-476/c
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LENGTH: 3434
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Aah85125 Human pro Aab39712 Prostate Ab195275 Human P77 Acc95439 Prostate Ad13326 Human pro Adg26342 Human pro Aef66623 Human pro

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Aah02724 Prostate
Aah84973 Human pro
Aaf86911 Human P77
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Abv43033 Human pro
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ALIGNMENTS

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L S	13-JUN-2000 (first entry)
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X OE	Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:311.
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2 5	number; propriet cancer; uragines; cumous; gene cherapy; decention;
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PF	14-JUL-1999; 99WO-US015838.
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PR	14-JUL-1998; 98US-00115453.
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PR	23-SEP-1998; 98US-00159822.
PR	15-JAN-1999; 99US-00232149.
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PR	09-APR-1999; 99US-00288946.
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E.	Dillon DC, Harlocker SL, Yuqiu J, Xu J, Mitcham JL;
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DR	WPI; 2000-171268/15.
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ᅜ	New polypeptide useful for treating and diagnosing prostate cancer
<u>Б</u>	comprises an immunogenic portion of prostate tumor protein.
X Z	J. Dage 100. 263mp. English
Ü	raye 133;

present invention describes isolated polypeptides, comprising an

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Result Š

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immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polynucleotides encoding them, antigen presenting cells which express the polypeptides, antibodies against the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or antibiotypic antibodies for passive immuno therapy. A portion of the polypurcleotides encoding the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAN06241 to AAA06691 and AAY82000 to AAY82202 represent sequences used in the exemplification of the present invention
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ive 0; Mismatches 0;
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The present invention describes polynucleotide sequences (I) which encode prostate appecific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. (I) and (II) can be used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AMM91357 to AMH93944 and AAM01115 to AAM01318 represent polymucleotide and amino acid sequences used in the exemplification of
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for use in
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                                                                                                                          Harlocker SL, Jiang Y, Reed SG;
Retter MW, Stolk JA, Skeiky YAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 525; DB 4; Length 526; 100.0%; Pred. No. 4.5e-115;
                                                                                                                                                                                                                        New polynucleotide encoding a prostate-specific protein, monitoring and treating prostate cancer in a patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                       Claim 1; Page 325; 543pp; English
                                                                                                                          Xu J, Dillon DC, Mitcham JL,
Kalos MD, Fanger GR, Day CH,
Wang A, Meagher MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 526; Conservative (
                              16-JAN-2001; 2001WO-US001574
                                                             14-JAN-2000; 2000US-00483672
                                                                                                                                                                                         WPI; 2001-425873/45
                                                                                             (CORI-) CORIXA CORP
19-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting calls expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting calls are useful for stimulating and/or expanding T calls specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is prostate specific polynucleotide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human prostate-specific polypeptides and polynucleotides useful for diagnosis and treatment of cancer, especially prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             relates to isolated prostate-specific polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kalos MD;
Carter D;
                                                                                                                                                                                                    Human; prostate cancer; ss; cytostatic; immunostimulant; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; DB 4; Length 526; 4.5e-115;
              AGTICTATAAACTGTAGTNTACTTATTTTAATCCCCAAAGCACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 525;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 327; 579pp; English.
                                                                                                                                                                          Human prostate cDNA sequence #304
                                                                                           BP.
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2000US-00570737.
2000US-00593793.
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2000US-00651236.
2000US-00657279.
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2000US-00709729
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Best Local Similarity 100.
Matches 526; Conservative
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09-AUG-2000;
29-AUG-2000;
06-SEP-2000;
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10-OCT-2000;
09-NOV-2000;
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12-MAY-2000;
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Li SX, Wa
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The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or its variant. (I) have cytostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynucleotides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the
                                                                                                                                                                                                                                                                               360
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                                                   CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA
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prostate cancer; immunogenic, cytostatic, vaccine; ss.
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development of cancer in a patient. Antibodies specific for prostate specific proteins and oligonucleotides that hybridise to a polynucleotide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression of a cancer, especially prostate cancer. AAH02422 to AAH2872, AAB7498 to AAB74821 and AAB74830 are sequences used in the exemplification of the present invention
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                                                                                                                 Length 526;
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                                                                                                                                        Indels
                                                                                            Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;
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Pred. No. 4.5e-115;
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                                                                                                                               Best Local Similarity 100.
Matches 526; Conservative
                                                                                                                              Similarity
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The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polynucleotides (N1) encoding (P1). (P1) and (N1) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P774P, P775P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region.

Prostate specific antigen (PSA) P501S was located on chromosome 1.

AAH84671 to AAH85143 and AAG99000 to AAG99077 represent polynucleotide and polypeptide sequences used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
                                                                                                                                                                                                                    Isolated polypeptide comprising at least an immunogenic portion of prostate-specific protein, useful in the diagnosis and therapy of
                                                                                                      Reed SG;
Wang A;
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                                                                                                        Harlocker SL, Jiang Y,
Day CH, Skeiky YAW,
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100.0%; Pred. No. 4.5e-115;
ive 0; Mismatches 0;
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                                                                                                        Mitcham JL, TW, Stolk JA,
99US-00439313
99US-00443686
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                                                                                                           Dillon DC, Mit
ID, Retter MW,
                                                                                                                                                                            WPI; 2001-308785/32.
                                                              (CORI-) CORIXA CORP
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Matches 526; Conserv
                                                                                                                                                                                                                                                                     prostate cancer.
12-NOV-1999;
18-NOV-1999;
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                                                                                                                                  Kalos MD,
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Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer.
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                 361 TCTCTTTACAGGGAGCTCCTGCAGCCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC
                                                            ACAGCAAGAGCTTCTCATCTAAACCCTTTCCCTTTTTAGTATCTGTGTATCAAGTATAAA
 361 TCTCTTTACAGGGAGCTCCTGCAGCCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC
                                                                                                                                                                                                                                                                                                                                                        Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein; immunogen; cancer; prostate specific antigen; PSA; prostatic acid phosphatase; PAP; prostate specific membrane antigen; PSMA; gene; ss.
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Carter D;
Hural J;
                                                                                                                                        AGTICTATAAACTGTAGTNTACTTATTTTAATCCCCAAAGCACAGT 526
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                                                                                                                                                                                                                                                                                                                             Prostate cancer therapy associated cDNA #303
                                                                                                                                                                                                                                  BP.
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04-OCT-2000; 2000US-00679272.
28-MAR-2001; 2001US-00822827.
                                                                                                                                                                                                                                  ACA59560 standard; cDNA; 526
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HOUGHTON R L.
Y DE BASSOLS C V.
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DBY C H.
VEDVICK T S.
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DILLON D C.
MITCHAM J L.
HARLOCKER S I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes compositions comprising peptides derived from the Wilm's tumour protein WT1 and methods for their use in treating malignant diseases. Peptides derived from both the murine and human WT1 proteins are provided. The human WT1 gene is found on chromosome 11p13, and the protein was shown to be a zinc finger transcription factor. The immunogenic peptides of the invention are particularly useful in the diagnosis and treatment of cancer and leukaemia. The present sequence is a coding sequence used in the exemplification of the invention
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                                                                                                                                         gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide comprising part of the Wilms Tumor gene product sequence is used in the diagnosis and treatment of malignant diseases e.g. leukemia and cancer associated with WTI.
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                                                                                                                                     Human; mouse; immunotherapy; cancer; leukaemia; WT1; Wilm's tumour chromosome 11p13; zinc finger transcription factor; ss.
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                                                                                                         Human P775P inventive antigen coding sequence SEQ ID NO: 336.
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                                                                            (first entry)
                 AAF86941 standard; cDNA;
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SKEIKY Y A W.
HEPLER W T.
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KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
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HARLOCKER S
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Li SX, War
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                   The invention describes a fusion protein comprising at least one amino acid sequence of immunogenic portions of any of the 3 sequences not defined in the specification, or sequences having at least 70 or 90 % sequence identity to any one of the 35 sequences defined in the USPTO web site, which is encoded by any of the 4 nucleotide sequences not defined in the specification. The fusion protein, composition and methods are useful for diagnosing, preventing and/or treating cancer, particularly prostate cancer. The proteins are useful as markers to indicate the presence or absence of cancer. This sequence represents a prostate cancer therapy associated cDNA. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at sequence. Last of the printed specifice at sequence.
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                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                               / Match 100.0%; Score 525; DB 5; Length 526; Local Similarity 100.0%; Pred. No. 4.5e-115; nes 526; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              526
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Example 3; SEQ ID NO 311; 85pp; English
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The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA described in the invention
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and as markers for the
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Best Local Similarity 100.0%; Pred. No. 4.5e-115;
Matches 526; Conservative 0; Mismatches 0;
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2000US-00483672.
2000US-0058857.
2000US-00568100.
2000US-005737.
2000US-00593793.
                                      97US-00806099.
97US-00904804.
98US-00030607.
98US-00115453.
98US-00159812.
99US-00232149.
99US-00232149.
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29-AUG-2000; 2000US-00651236.
06-SEP-2000; 2000US-00657279.
02-OCT-2000; 2000US-00679426.
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                                         TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATTATATTATCTA
                                                               TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATTATATTATCTA
                                                                                                                                           CATTTACAGCATTTAAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAAATAA
                                                                                                                                                                                                                                      <u> ATTAAACATGGAATAAAGATTTGTCCTTAAATATATCTACAAGAAGACTTTGATATTTG</u>
                                                                                                                                                                                                                                                                                                     TTTTTCACAAGTGAAGCATTCTTATAAAGTGTCATAACCTTTTTGGGGAAACTATGGGGAA
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    CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC
                                                                                                                     CATITIACAGCATITIAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA
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29-JUN-2001; 2001US-00895814.
10-DEC-2001; 2001US-00012896.
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Carter D, Li
Mcneill PD,
Deng T,
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The present invention relates to novel prostate-specific proteins (PSP) and their coding sequences. The PSPs and their coding sequences are useful for stimulating an immune response in a patient, or for treating prostate cancer in a patient and for determining, detecting or diagnosing the presence of a cancer in a patient. The present sequence was used to
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Pred. No. 4.5e-115;
O; Mismatches O;
Example 3; Page 392-393; 691pp; English.
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                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Watches 526; Conservative
                                                                                                                                                                   illustrate the invention
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The invention relates to an isolated polypeptide comprising no more than 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The peptides comprise a fragment ADB13563 of that contain naturally processed T-cell epitopes for 3 class I major histocompatibility complex (MHC) alleles. ADB13563 is a polypeptide encoded by a human prostate specific CDMA, one of 648 disclosed as new. Also included are nucleic acids encoding the proteins and peptide, expression vectors, a host cell transformed with the vector, an isolated antibody (or antigen binding crassence of a cancer in a patient (comprising contacting a patient sample with a binding agent that binds to the protein or peptide, detecting the amount of polypeptide to a predetermine comparing the amount of polypeptide to a predetermined cutoff value to determine the presence of cancer), a fusion protein of value to determine the presence of cancer), a fusion protein comprising the peptides or proteins, stimulating or expanding T cells specific for a tumour protein comprising contacting T cells with the peptides or the isolated T cell population, treating prostate cancer in a patient and treating prostate cancer in a patient and treating prostate cancer in a patient and treating prostate cancer in a patient with the peptides or compounds, determining the presence of a cancer in a patient with the peptides or antigen presenting clust express (the peptides to that the T cells proliferate, and administering the contacting cluster of differentiation (CD4+) and/or CD8+ T cells isolated concerning cluster of differentiation (CD4+) and/or of detect the contacting cells expressing the moteled acids encoding, or antigen-presenting cells expressing the nucleic acids encoding, or antigen-presenting cells represented the peptides or antigen-presenting cells expressing the nucleic acids encoding, or antigen-presenting cells concerning cluster. The peptides or antigen-presenting cells concerning cells expressing the nucleic acids encoding, or antigen-presenting cells expr
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2000US - 00657279.
2000US - 00679426.
2000US - 00685166.
2001US - 00759143.
                                                                                                                                98US-00030607.
98US-00115453.
98US-00159812.
99US-00288946.
99US-00352616.
99US-00433613.
2000US-00443686.
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29-JUN-2001; 2001US-00895814.
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2000US-00570737
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2000US-00605783.
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                                    2002US-00294025
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12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
09-AUG-2000;
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13-JUL-1999;
12-NOV-1999;
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                                                                                                                                                                                                                                                                                      TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATTATATTATCTA 120
                     or antigen
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stimulate or expand T cells specific for a tumour protein. The peptides, nucleic acids, antibodies, fusion proteins, T cell populations or antige presenting cells are used to stimulate an immune response or treat prostate cancer in a patient. The present sequence is one of the disclosed human prostate specific CDNAs. Note: Except where otherwise indicated, the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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                                                                                                          from USPIO at segdata.uspto.gov/seguence.html?DocID=20030185830
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                                                                                                                                       Sequence 526 BP; 177 A; 92 C; 86 G; 170 T; 0 U; 1 Other;
                                                                                                                                                                  100.0%; Score 525; DB 10;
100.0%; Pred. No. 4.5e-115;
ative 0; Mismatches 0;
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                                                                                                                                                                                                 526; Conservative
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                  CATTTACAGCATTTAAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA
                                                                      TITITCACAAGTGAAGCATICTTATAAAGTGTCATAACCTTTTTGGGGAAACTATGGGAA
                                                                                                                                                                                                                                                                     ACAGCAAGAGCTTCTCATCTAAACCCTTTCCCTTTTTAGTATCTGTGTATCAAGTATAAA
    CATTTACAGCATTTAAAATGTGTTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA
                                                       ATTAAACATGGAATAAAGATTTGTCCTTAAATATAATCTACAAGAAGACTTTGATATTTG
                                                                                                                                                             AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC
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Day CH, Vedvick TS;
                                                                                                                                                                                                                                                                                                                          AGTICIATAAACTGTAGINTACTTATTTTAATCCCCAAAGCACAGT
                                                                                                                                                                                                                                                                                                                                      Human prostate tumor cDNA clone P775P, SEQ ID 311.
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970S-00904804.
980S-00020607.
980S-00115453.
980S-00159812.
990S-00232149.
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2000US-00483672.
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09-MAY-2000; 2000US-00568100
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27-MAR-2000;
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09-APR-1999;
13-JUL-1999;
12-NOV-1999;
18-NOV-1999;
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25-FEB-1998;
14-JUL-1998;
23-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   protein comprising a prostate-specific polypeptide. The sequences of the invention are used to diagnose and treat cancer, particularly prostate cancer. This sequence represents cDNA encoding a human prostate-specific polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at sequence.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding prostate specific polypeptides isolated from a human prostate tumor cDNA library are useful to diagnose and treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human prostate-specific polypeptides and the polynucleotides encoding them. The invention also relates to an isolated antibody or its antigen-binding fragment that specifically binds a polypeptide of the invention, a method of detecting cancer in a patient comprising contacting a biological sample of the patient with an agent that binds a prostate-specific polypeptide and comparing the amount of bound polypeptide compared to a predetermined cut-off value and a fusion
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Day CH, Vedvick TS;
oler WT, Hural J;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, He Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedv Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural Mcneill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Meagher MJ, Deng T;
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970S-00806099.
970S-00904804.
980S-00030607.
980S-0015453.
980S-0015453.
980S-0015453.
990S-00158946.
990S-0035616.
990S-0043913.
2000US-00593793.
2000US-00593793.
2000US-00593793.
2000US-00593793.
2000US-00593793.
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2001US-00759143.
2001US-00780669.
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Matches 526; Conservative
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14-JAN-2000;
27-MAR-2000;
09-MAY-2000;
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06-SEP-2000;
02-OCT-2000;
10-OCT-2000;
09-NOV-2000;
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29-JUN-2001;
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23-SEP-1998;
15-JAN-1999;
09-APR-1999;
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09-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                 10-DEC-2001;
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13-JUN-2000;
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                                                                                                         13-JUL-1999;
                                        25-FEB-1998
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                                                 The present invention relates to prostate-specific fusion proteins and DNA encoding sequences. The fusion proteins can be used for diagnosing, preventing, or treating cancer, such as prostate cancer. The prostate specific proteins were isolated from a human prostate tumor cDNA library. The present sequence is one such cDNA clone which was isolated in the prostate-specific CDNA library. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
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 treating cancer,
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                                                                                                                                                                      ; Score 525; DB 15;
; Pred. No. 4.5e-115;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human prostate expression marker cDNA 27587
useful for diagnosing, preventing,
                               Example 3; SEQ ID NO 311; 78pp; English
                                                                                                                                                                       100.0%;
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) assessing the prostate call carcinogenic potential of a compound; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1203 BP; 395 A; 209 C; 199 G; 391 T; 0 U; 9 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTC
                                                                                                                                                                                                                                                                               INC.
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                                                                                                                                                                                                                                                                                                                                             Monahan JE;
                                                       17-FEB-2000; 2000US-0183319P.
16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
09-UNN-2000; 2000US-0211314P.
13-DEC-2000; 2000US-021519P.
20-FEB-2001; 2001WO-US005171
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Matches 512; Conservative
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether
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                                                                                                                                                                                                                                                                                           642 AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC
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                                           CATITACAGCATITAAAATGIGITICAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA
                                                                                                                                        522 ATTAAACATGGAATAAAGATTTGTCCTTAAATATATATCTACAAGAAGACTTTGATATTTG
                                                                                                                                                                                   TTTTTCACAAGTGAAGCATTCTTATAAAGTGTCATAACCTTTTTGGGGAAACTATGGGAA
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                                                                                                                                                                                                                                                                 AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC
                   CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA
                                                                                                 ATTAAACATGGAATAAAGATTTGTCCTTAAATATATAATCTACAAGAAGACTTTGATATTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTICTATAAACTGTAGINTACTTATTTTAATCCCCAA 518
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2000US-0207454P.
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pharmacogenomic marker;
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25-MAY-2000;
09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                 Human, prostate cancer, cytostatic; carcinogen, pharmacodyanamic marker, pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
ATAGC-AGAGCTTCTCATCTAAACCCTTTTCCCTTTTTAGTGTCTGTGTATAC-AGTATAAA
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                                                              AGTTCTATAAACTGTAGT-TACTTATTTAATCCCAAA
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2000US-0207454P.
2000US-0211314P.
2000US-0219007P.
                                                                                                                                                                                   standard; cDNA; 1203
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a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
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90.9%; Score 477.2; DB 5;
Best Local Similarity 98.8%; Pred. No. 1.2e-103;
Matches 512; Conservative 0; Mismatches 3;
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Search completed: December 31, 2006, 12:54:20 Job time : 409.854 secs AC080000 Homo sapi AC080181 Homo sapi

AL512624 Human chr

OM nucleic

Run on:

Sequence:

Searched:

Database

Result No.

87654321098765432

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BD242216 52003 Sold by DNA linear PAT 17-JUL-2003 Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use.
                                             CQ48898 Sequence
CQ49668 Sequence
CQ496503 Sequence
CQ495743 Sequence
AL59182 Human chr
AD00528 Human chr
AD00528 Homes api
CQ511185 Sequence
BV57126 G591P6332
AR278575 Sequence
AR40307 Sequence
AR40307 Sequence
AR58940 Sequence
AR58940 Sequence
AR58990 Sequence
AR58990 Sequence
AR68990 Sequence
AR6870099 Sequence
AR117006 Sequence
AX140986 Sequence
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PN JP 2005220054-A/303
PD 09-JUL-2002
PF 14-JUL-1999 US 09/159822, 23-SEP-1998 US 09/159812 PR
13-SEP-1999 US 09/222880,15-JAN-1999 US 09/159812 PR
15-JAN-1999 US 09/22880,15-JAN-1999 US 09/232149 PR
PI DAVIN CLIFORD DILLON, SUSAN LOUISE HARLOCKER, JIANG YUQIU, PI
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C12N15/09,A61K38/00,A61K39/00,A61K39/395,C07K14/47,C07K16/30,
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C12P21/08,C12Q1/68,G01N33/574,G01N33/68//A61P35/00,C12N15/00,
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (Dases 1 to 526)

1 (Dases 1 to 526)

Dillon, D.C., Harlocker, S.L., Yuqiu, J., Xu, J. and Mitcham, J.L.

Compounds for immunotherapy and diagnosis of prostate cancer and methods for their use

Patent: JP 2002520054-A 303 09-JUL-2002;

CORIXA CORP
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    .526
    /organism="Homo sapiens"

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BD242216.1 GI:33051986
JP 2002520054-A/303.
Homo sapiens (human)
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9932.518 Million cell updates/sec
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                                                                                                                     December 31, 2006, 12:13:09 ; Search time 3386.49 Seconds
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Copyright (c) 1993 - 2006 Biocceleration Ltd
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Corixa Corporation; Seattle, WA
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Location/Qualifiers
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                                                              100.0%; Score 525; DB 2; L
Larity 100.0%; Pred. No. 2.3e-138;
Conservative 0; Mismatches 0;
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Xu,J., Dillon,D.C. and Mitcham,J.L.
Compounds for immunotherapy of prostate
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Patent: US 6465611-A 311 15-OCT-2002;
Corixa Corporation; Seattle, WA
Location/Qualifiers
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 2 AR237399 LOCUS

ORGANISM REFERENCE AUTHORS source

ORIGIN

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FEATURES

JOURNAL

TITLE

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Db 241 TTTTCACAAGTGAAGCATTCTTATAAAGTGTCATAACCTTTTTGGGGAAACTATGGGAA 300	Oy 301 AAAATGGGGAAACTCTGAAGGGTTTTAACTATCTTACCTGAAGCTACAGACTCCATAACC 360	0y 361 TCTCTTTACAGGAGCTCCTGCAGCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420	Oy 421 ACAGCAAGAGCTTCTCATCTAAACCTTTCCCTTTTAGTATCTGTATCAAGTATAAA 480	OY 481 AGTTCTATAAACTGTAGTNTACTTATTTTAATCCCCAAAGCACAGT 526	AR371015	TION Sequence 311 from patent US 6395278. ION AR371015 DS	SOURCE Unknown. ORGANISM Unknown. ORGANISM Unknown. The control of the control	FEATURES Location/Qualifiers 1. 526 /organism="unknown" /mol type="qenomic DNA"	ORIGIN Query Match 100.0%; Score 525; DB 2; Length 526; Rest Local Similarity 100.0%; Pred. No. 2.3e-138;	Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps	OY 1 CAANTITGAGCCAATGACATKAGAATTITACAAAAAGCTTATTCTGGGGCCATTTC 60	Qy 61 TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATTATATTATTTA 120	Oy 121 CATTTACAGCATTTAAAATGTCTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180 121 CATTTACAGCATTTAAAATGTCTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180	181 ATTAAACATGGAATAAACATTTGTCCTTAAATATAATCTACAAGAACACTTTGATATTTG	241 TITITCACAAGTGAAGCATTCTTATAAAGTGCATAACCTTTTTGGGGAAACTATGGGAA 241 ATTTTCACAAGTGAAGCATTCTTATAAAGTGCATAACCTTTTTGGGGAAACTATGGGAA 241 ATTTTCACAAACCAATAATAAAAAACTGCAAAACTGCAAAAAAAA	301 AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC	
	Oy 181 ATTAAACATGGAATAAAGATTTGTCCTTAAATATAATCTACAAGAAGACTTTGATATTTG 240	OY 241 TITITCACAAGIGAAGCAITCTIAIAAAGIGICAIAACCTITITGGGGAAACTAIGGGAA 300 	OY 301 AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360 	Oy 361 TCTCTTTACAGGGGGCTCCTGCAGCCCTACAGAATGAGTGGCTGAGATTCTTGATTGC 420	Qy 421 ACAGCAAGACTTCTCATCTAAACCCTTTCTTAGTATCTGTGTATCAGTATAAA 480 	Oy 481 AGTTCTATAAACTGTAGTNTACTTATTTTAATCCCCAAAGCACAGT 526 	RESULT 4 AR367119 LOCUS LOCUS AR367119 LOCUS AR367119 LOCUS AR367119 ACCESSION AR367119	_	AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Yugiu,J., Reed,S.G., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A. and Day,C.H. Compositions and methods for therapy and diagnosis of prostate	Ab Patent: US 6329505-A 311 11-DEC-2001;	Corixa Corporation, Seattle, WA FEATURES Location/Qualifiers source 1. 526	/organism="unknown" /mol_type="genomic DNA"	<pre>Query Match</pre>	1 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60 	Oy 61 TTTTGACGTTTTCTCTAAACTACTAAAGGGCATTAATGATCCATAAATTATATTATCTA 120 	121 CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180 	181 ATTABACATGGAATABAGATTTGTCCTTBAATATATATCTACAAGAAGACTTTGATATTTG 240

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Best Local Similarity 100.0%; Pred. No. 2.3e-138;
Matches 526; Conservative 0; Mismatches 0;
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Corixa Corporation; Seattle, WA;
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Sequence 311 from patent
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., L., Xx., Wang,A., Skeiky,Y.A.W., Hepler,W.T. and Henderson,R.A.

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Llarity 100.0%; Pred. No. 2.3e-138;
Conservative 0; Mismatches 0;
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Corixa Corporation; Seattle, WA
Location/Qualifiers
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/organism="unknown"
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvic,Y.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
Hepler,W.T. and Henderson,R.A.
Compositions and methods for the therapy and diagnosis of prostate
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       Hepler, W.T. and Henderson, R.A. Compositions and methods for the therapy and diagnosis of cancer
//edvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
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Best Local Similarity 100.0%; Pred. No. 2.3e-138;
Matches 526; Conservative 0; Mismatches 0;
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Corixa Corporation; Seattle, WA
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Corixa Corporation; Seattle, WA
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Sequence 311 from patent 1
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
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Matches 526; Conservative 0; Mismatches 0;
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Corixa Corporation; Seattle, WA;
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 9 AR563802 LOCUS

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Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 CADAITTGAGCCAATGACATTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60		121 CATTIACAGCATTTAAAATGIGIILAGCALGAAATATTAGCLACAGGGGAGGCTAAATAA 181 ATTAAACATGGAATAAAGATTTGTCCTTAAATATAATCTACAAGAAGACTTTGATATTTG		301 AAAATGGGGAAACTCTGAAGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 301 AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTAAAGAGACTCTAAACG	361	421 ACAGCAAGAGCTTCTCATCTAAACCCTTTCCCTTTTTAGTATCTGTGTGTG	481 AGTICTATAAACTGTAGTNIACTTATTTAATCCCAAAGCACAG 526	SULT 12	AR655947 LOCUS AR656947 526 bp DNA linear PAT 13-JUN-2005 DEFINITION Sequence 311 from patent US 6894146. ACCESSION AR656947 VERSION AR656947.1 GI:67590059	Unknow Unclass Unclass 1 (ba Xu,J.; Kalos; Vedvic Hepler Compos cancer	Corixa Corporation; Seattle, WA FEATURES Location/Qualifiers source 1. :526 /organism="unknown" /mol_type="genomic DNA"	Query Match 100.0%; Score 525; DB 2; Length 526; Best Local Similarity 100.0%; Pred. No. 2.3e-138; Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Oy 1 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60	OY 61 TITIGACGTTITCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATTATATTATCTA 120
1526 /organism="unknown" /mol_type="genomic DNA" 100.0%; Score 525; DB 2; Length 526;	vative 0; Misr GCCAATGACATAGAATT GCCAATGACATAGAATT	Qy 61 TTTTGACGTTTTCTCTAAACTACTAAGGGCATTAATGATCCATAAATTATATTATCTA 120 	Oy 121 CATITACAGCATITAAAATGIGITCAGCATGAAATAITAGCIACAGGGGAAGCIAAATAA 180 	Qy 181 ATTAAACATGGAATAAAGATTGTCCTTAAATATAATCTACAAGAAGACTTTGATATTTG 240 	Qy 241 TTTTCACAAGTGAAGCATTCTTATAAAGTGTCATAACCTTTTTGGGGAAACTATGGGAA 300 	Oy 301 AAAATGGGGAAACTCTGAAGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360	OY 361 TCTCTTTACAGGAGCTCCTGCAGCCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC 420	Qy 421 ACAGCAAGAGTTCTCATCTAAACCCTTTCCTTTTTAGTATCTGTGTATCAAGTATAAA 480 Db 421 ACAGCAAGAGCTTCTCATCTAAACCCTTTTCCCTTTTTAGTATCTGTGTATCAAGTATAAA 480	Qy 481 AGTTCTATAAACTGTAGTNTACTTATTTTAATCCCCAAAGCACAGT 526 	RESULT 11 AR605608 LOCUS DEFINITION Sequence 311 from patent US 6818751. ACCESSION AR605608 VERSION AR605608.1 GI:56657272 SOURCE UNCHOWN. ORGANISM Unchaesified. REFERENCE 1 (bases 1 to 526)	Xu,J., Kalos,N Vedvick Hepler, Composi	OUDWAND FATENT: US BEBS/3-A 311 IS-NOV-2004; PEATURES Location/Qualifiers Source 1. 526	iganism≡ unxnown: ol_type="genomic DNA"	Query Match 100.0%; Score 525; DB 2; Length 526; Best Local Similarity 100.0%; Pred. No. 2.3e-138;

181 ATTAAACATGGAATAAAGATTTGTCCTTAAATATAATCTACAAGAAGACTTTGATATTTG 240 	241 TITITCACAAGTGAAGCATTCTTATAAAGTGTCATAACCTTTTTGGGGAAACTATGGGAA 300	241 TTTTCACAAGTGAAGCATTCTTATAAAGTGTCTTAAACCTTTTTGGGAAACTTATGGGAA 300 301 AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360	301 AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 360 361 TCTCTTTACAGGAGCTCCTGCAGCCCCTACAGAAAGAGTGGCTGAGAATTCTTGATTGC 420		421 ACAGCAAGAGCTTCTCATCTAAACCCTTTCCCTTTTAGTATCTGTGTATCAAGTATAAA 480			AX106198 N Sequence 336 AX106198	_	FERENCE 1 AUTHORS Skeiky,Y.A., Xu,J., Cheever,M.A. and Reed,S.G. TILE Compositions and methods for wtl specific immunotherapy JOURNAL Patent: WO 0125773-A 336 12-APR-2001;	rce	n="Homo sapi =="unassigne ="taxon:9606	/note="n = A,T,C or G" .	Query Match 100.0%; Score 525; DB 2; Length 526; Best Local Similarity 100.0%; Pred. No. 2.3e-138; Matches 526; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 CAAATTTGAGCCAATGACATTTTACAAATCAAGAGCTTATTCTGGGGCCATTTC 60	1 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 60	TITICACGITITCICTAAACTA TAAACAGCATTAA LOATCATAAATATATCIA TITITGACGITITCICTCTAAACTACTAAGAGGCATTAATGATCCATAAATTATATTATCTA	121 CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGAAGCTAAATAA 180	121 CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGAAGCTAAATAA 180 181 ATTAAACATGGAATAAAGATTTGTCCTTAAATATAAATGTACAAGAAGACTTTGATATTTG 240		241 TTTTCACAAGTGAAGCATTCTTATAAAGTGTCATAACCTTTTTGGGGAAACTATGGGAA 300
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	Db 121 CATTTACAGCATTTAAAATGTGTTCAGCATGAAATTTAGCTACAGGGGAAGCTAAATAA 180	OY 181 ATTAAACATGGAATAAAGATTTGTCCTTAAATATAATCTACAAGAAGACTTTGATATTTG 240	Qy 241 TITITCACAAGTGAAAGCATTCTTATAAAGTGTCATAACCTTTTTGGGGAAACTATGGGA 300 Db 241 TITITCACAAGTGAAGCATTCTTATAAAGTGTCATAAACTGTCATAAACTGTCATAAAAAAAA	AAAATGGGGAAACTCTGAAGGGTTTTTAAGTATCTTACCTGAAGGTACGATAACC	301 AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACTGCAATGTCATACT 261 GCGGGAAACTCCAACAGGGGTTTAAGTATCTTACCTGAAGCTACAAGTGATACTTAACTAAGGGTTAAAGGTTAAAGGGT	DD 361 TCTCTTTACAGGGAGCTCCTGCAGCAGTACAGAAATGAGGGCTGAGATTGC 420	Qy 421 ACAGCAAGAGCTTCTCATCTAAACCCTTTTCTTAGTATCTGTGTATCAAGTATAAA 480 Db 421 ACAGCAAGAGCTTCTCATCTAAACCCTTTTTAGTATCTGTGTATCAAGTATAAA 480	481 AGTTCTATAAACTGTAGTNTACTTATTTTAATCCCCAAAGCACAGT 526 	AR716854 LOCUS LOCUS AR716854 AR716854 S26 bp DNA linear PAT 07-OCT-2005 DEFINITION Sequence 311 from patent US 6943236. ACCESSION AR716854 VERSION AR716854.1 GI:77365503	KEYWORDS SOURCE Unknown. ORGANISM Unknown. Unclassified.	REFERENCE 1 (bases 1 to 526) AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,	Vedvick, T.S., Carter, D., Li, S.X., Wang, A., Skeiky, Y.A.W., Hepler, W.T., Henderson, R.A., Hural, J., McNeill, P.D., Houghton, R.L., Vinals y de Bassole, C., Foy, T.W., Watanabe, Y. and Meagher, M.J. TITLE Compositions and methods for the therapy and diagnosis of prostate	Cancer: US 6943236-A 311 13-SEP-2005; Corixa Corporation: Seattle, WA	FEATURES Location/Qualifiers source 1.:526 /organism="unknown"	/mol_type="genomic DNA"	icore 525; DB 2; Length 526; red. No. 2.3e-138; Minniphon 0. Indol	n	Db 1 CAAATTTGAGCCAATGACATAGAATTTACAAATCAAGAAGCTTATTCTGGGGGCCATTC 60	OY 61 TTTTGACGTTTTCTCTAAACTAAAGGGCATTAATGATCCATAAATTATATTATTATT 120	121 CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAAATAA	Db 121 CATTTACAGCATTTAAAATGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180

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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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CORIXA CORPORATION (US)
Location/Qualifiers
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/mol_type="unassigned DNA"
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Listing first 45 summaries
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u	311, App 476, App	475, App	458,	732, App	746, App	, 2856, Ap	606, App	346, App	290, App	564, App	9, Appli	19, Appl	174,	302,	29044, A	e 73, Appl		472,	287, App	207, App
Description	Sequence	Sequence	Sequence	Sequence 732,	Sequence	Sequence	Sequence 606	Sequence	Seguence	Sequence	Seguence	Sequence	Seguence	Seguence	Sequence 29044	Sequence 73,	Sequence 706,	Seguence	Sequence	Sequence
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	33	40	7.6	5286	9	US-10-517-441-568	Sequence 568, App
O	34	40	7.6	365720	9	US-10-669-920-1267	•
υ	35	39.8	7.6	894	7	US-11-204-780-6524	Sequence 6524, Ap
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	39	39.6	7.5	342748	9	US-10-669-920-1313	Sequence 1313, Ap
	40	39.5	7.5	3883	σ	US-11-218-305-7775	Sequence 7775, Ap
υ	41	39.2	7.5	6432	9	US-10-517-441-332	Sequence 332, App
υ	42	39.2	7.5	6432	Q	US-10-506-111-218	Sequence 218, App
υ	43	39.2	7.5	338780	φ	US-10-669-920-1211	Sequence 1211, Ap
υ	44	39	7.4	438	2	US-11-292-078-6304	Seguence 6304, Ap
	45	39	7.4	848	7	US-11-204-780-5907	Sequence 5907, Ap

ALIGNMENTS

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Sequence 311, Application US/11344932
Publication No. US2006026933A1
GENERAL INPORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Millon, Davin C.
APPLICANT: Michael D.
APPLICANT: Michael D.
APPLICANT: March M. Osmifer L.
APPLICANT: Kalos, Michael D.
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APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
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                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 525; DB 7; Length 526; 100.0%; Pred. No. 4.1e-122; Live 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: 09/759,143
PRIOR FILING DATE: 2001-01.12
PRIOR PILING DATE: 2001-01.12
PRIOR FILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-10.10
PRIOR PILING DATE: 2000-10.10
PRIOR PRIOR DATE: 2000-10.02
PRIOR APPLICATION NUMBER: 09/679,426
PRIOR PILING DATE: 2000-10-02
PRIOR PILING DATE: 2000-09-06
Remaining Prior Application data removed - St
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: PASESEQ for Windows Version 3.0
SERIOTH: 526
                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: 499
CTHER INFORMATION: n = A,T,C or US-11-344-932-311
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 526, Conservative
                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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US-11-344-932-476/C

Sequence 476, Application US/11344932

Publication No. US20060269532A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.

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3062 CAAATTTGAGCCAATGACATTAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 3003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ë,
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APPLICANT: Hural, John
APPLICANT: Mowell, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Winals y de Bassols, Carlota
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Deng, TB
APPLICANT: Deng, TB
APPLICANTON UNDERS: US/11/344,932
CURRENT APPLICATION NUMBER: US/11/344,678
RRIOR APPLICATION NUMBER: 10/012,896
RRIOR PILING DATE: 2001-05-09
RRIOR PILING DATE: 2001-06-29
RRIOR APPLICATION NUMBER: 09/895,814
RRIOR APPLICATION NUMBER: 09/895,814
RRIOR APPLICATION NUMBER: 09/895,814
RRIOR APPLICATION NUMBER: 09/780,669
RRIOR APPLICATION NUMBER: 09/780,709
RRIOR APPLICATION NUMBER: 09/685,166
RRIOR APPLICATION NUMBER: 09/685,166
RRIOR APPLICATION NUMBER: 09/679,426
RRIOR APPLICATION NUMBER: 09/679,426
RRIOR APPLICATION NUMBER: 09/679,426
RRIOR APPLICATION NUMBER: 09/677,279
RRIOR PILING DATE: 2000-10-00
RRIOR PILING DATE: 2000-10-00
RRIOR PILING DATE: 2000-00-06
RRIOR PILING DAT
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                                                                                                                                                                                           Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
                                                                                                                                                                                                                                                                                                                                                        Skeiky, Yasir A. W.
Hepler, William T.
Jiang, Yuqiu
Henderson, Robert
Kalos, Michael D.
                                                                                             Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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CORGANISM: Homo sapiens
US-11-344-932-476
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PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: 09/679,426
PRIOR PILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR APPLICATION NUMBER: 09/657,279
PRIOR PILING DATE: 2000-09-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1033
SOFTWARE: PSEUSEQ For Windows Version 3.0
LENGTH: 2414
                                                                                                                                                                                                                                                                                                                                                                                                                         49.8%; Score 261.6; DB 7; Length 2414; 98.1%; Pred. No. 7.3e-56; Indels 0; Mismatches 5; Indels 0;
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Publication No. US20060269532A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: n = A,T,C or G
US-11-344-932-475
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Meagher, Madeleine Joy
Deng, Ta
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Houghton, Raymond L.
Vinals y de Bassols, C
Foy, Teresa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harlocker, Susan L.
Jiang, Yugiu
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Hepler, William T.
Hural, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 98.13
Matches 264; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Samuel X.
                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: 33
                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang, Aijun
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                        2762 AAAATGGAGAAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC 2703
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    2882 ATTAAACATGGAATAAAGATTTGTCCTTAAAAATAATCTACAAGAGAGTCTTGATATTTG 2823
                                                                                                                                                                                                                                                                                                                                 480
                                                   300
                                                   TITITCACAAGTGAAGCATICTTATAAAGTGTCATAACCTTTTTGGGGAAACTATGGGAA
                                                                                            2822 TITITCACAAGIGAAGCATICITATAAAGIGICATAACCITITITGGGGAAACTAIGGGAA
                                                                                                                                                                                                                                                                  2702 TCTCTTTACAGGGAGCTCCTGCAGCCCCTACAGAAATGAGTGGCTGAGATTCTTGATTGC
                                                                                                                                                                                                                                                                                                                                 421 ACAGCAAGAGCTTCTCATCTAAACCCTTTTCCCTTTTTAGTATCTGTGTATCAAGTATAAA
                                                                                                                                        301 AAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCATAACC
                                                                                                                                                                                                                                     361 TCTCTTTACAGGAGCTCCTGCAGCCCCTACAGAATGAGTGGCTGAGATTCTTGATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C32 CURRENT APPLICATION NUMBER: US/11/344,932 CURRENT FILING DATE: 2006-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2584 AGTTCTATAAACTGTAGT-TACTTATTTTAATCCCAAA 2548
                                                                                                                                                                                                                                                                                                                                                                                                                            481 AGTICTATAAACTGTAGTNIACTTATTTAATCCCCAA 518
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Houghton, Raymond L.
Vinals y de Bassols, Carlota
Foy, Teresa M.
Watanabe, Yoshihiro
Meagher, Madeleine Joy
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RRIOR FILING DATE: 2002-05-09
RRIOR FILING DATE: 2002-05-09
RRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 10/012,896
PRIOR APPLICATION NUMBER: 09/895,814
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-09
PRIOR PRIOR DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 09/780,669
PRIOR APPLICATION NUMBER: 09/789,143
PRIOR APPLICATION NUMBER: 09/799,143
PRIOR PELLING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-12
PRIOR FILING DATE: 2001-01-10
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US-11-344-932-475/c
Sequence 475, Application US/11344932
; Publication No. US20060269532A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Jiang, Yuqiu APPLICANT: Henderson, Robert A. APPLICANT: Kalos, Michael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang, Aijun
Skeiky, Yasir A. W.
Hepler, William T.
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Vedvick, Thomas
Carter, Darrick
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Retter, Marc W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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AFPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT APPLICATION NUMBER: D01-11
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR PILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR FILING DATE: 2003-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2161 ITTAATTTTAAAATAAAATAAAATAAAATAACTATTACATACGAAAATATACATTAATT 2102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 ITTICICIDAAACIACIAAAAGAGGCAITAAIGAICCAIAAATIAITAITAICAATITACA
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                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 4022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
8.7%; Score 45.8; DB 6; Length 4
Best Local Similarity 51.2%; Pred. No. 0.11;
Matches 107; Conservative 0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1981 AAATCAAATTTTAATTAAAATTATCATAA 1953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 AAGTGAAGCATTCTTATAAAGTGTCATAA 277
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: DE 10300096.8
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2002-10-01
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 458
LENGTH: 4022
                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: unsure

CCATION: (1299, 1372, 1784, 3008, 3018)

CTHER INFORMATION: unknown base

US-10-517-441-458
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Publication No. US20060121467A1
GENERAL INFORMATION:
APPLICANT: FOEKENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
APPLICANT: MARIER, Sabine
APPLICANT: MARIER, John
APPLICANT: MODEL, Fabian
                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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SCHMITT, Manfred
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RUJAN, Tamas
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SEQ ID NO 732
LENGTH: 4022
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APPLICANT:
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TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE: 47675-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 50
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 474
LENGTH: 1594
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  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REPERENCE: 210.21.47.032 CURRENT APPLICATION NUMBER: US/11/344,932 CURRENT FILING DATE: 2006-02-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITIGACGITITICICIAAACTACTAAAGAGGCATTAATGAICCATAAAT 109
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CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION UNMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
                                                                                                                             PRIOR APPLICATION NUMBER: 10/144,678
PRIOR FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: 10/012,896
PRIOR APPLICATION NUMBER: 09/095,814
PRIOR APPLICATION NUMBER: 09/095,814
PRIOR PAPLICATION NUMBER: 09/095,814
PRIOR FILING DATE: 2001-06-09
PRIOR FILING DATE: 2001-06-09
PRIOR FILING DATE: 2001-05-09
PRIOR PELICATION NUMBER: 09/780,669
PRIOR APPLICATION NUMBER: 09/799,143
PRIOR APPLICATION NUMBER: 09/79,143
PRIOR PILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/79,143
PRIOR PILING DATE: 2000-11-09
PRIOR PILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: 09/659,426
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-10-09
PRIOR FILING DATE: 2000-00-02
PRIOR FILING DATE: 2000-00-02
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Publication No. US20060121467A1
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SCHMITT, Armin
SCHMITT, Manfred
LOOK, Maxime P.
MARX, Almuth
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KOENIG, Thomas
MAIER, Sabine
MARTENS, John
MODEL, Fabian
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US-11-344-932-474
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APPLICANT:
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APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
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APPLICANT: Kreps, Joel
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APPLICANT: Wann
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCALP1300-3
CURRENT APPLICATION NUMBER: US/11/299,286
CURRENT PILING DATE: 2005-12-09
PRIOR PELICATION NUMBER: US 60/227,866
PRIOR PELICATION NUMBER: US 60/227,866
PRIOR PELICATION NUMBER: US 60/264,647
PRIOR PELICATION NUMBER: US 60/264,647
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                            9739 ATTTTTTTTTTTTTTTTAATTATATATTTAAGAATGTAAATTGTGATTAGATTTATTT 9798
                                                                                                                                                                                                                                                                                                                   9799 ATATTTTTAGAATATTATGAAATGTGTTTTAAATATGTTAATTGATTGATTTAGAAATTTT 9858
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                                                                                                       1311 TTGAGTATTATTGATTTTTATAAATCATATCAAAAAGTTCAAAATATTTTTAATCTAAA 1252
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                                                      94 TTAATGATCCATAAATTATATTATCTACATTTACAGCATTTAAAATGTGTTCAGCATGAA
                                                                                                                                                           154 ATATTAGCTACAGGGAAGCTAAATAAATTAAACATGGAATAAAGATTTGTCCTTAAATA
                                                                                                                                                                                                                                                                  214 TAATCTACAAGAAGACTTTGATATTTGTTTTTCACAAGTGAAGCATTCTTATAAAGTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 TCTACATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAA
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87; Indels
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8.1%; Score 42.4; DB 10;
Best Local Similarity 49.1%; Pred. No. 0.62;
Matches 112; Conservative 0; Mismatches 116;
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2856, Application US/11299286; Publication No. US20060183137A1; GENERAL INFORMATION:
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; Sequence 606, Application US/10517441
; Publication No. US20060121467A1
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     95; Conservative
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     Matches
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TITLE OF INVENTION: proliferative disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                        2161 TTTAATTTTAAAAATAAAATACATAAAATAACTATTACATACAAAAATATACATTAATT 2102
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                                                                                                                                                                                                                                                                                                                                                                       TTTTCTCTAAAACTACTAAAAGAGGCATTAATGATCCATAAATTATATTATTATATTTACA 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 TGGAATAAAGATTTGTCCTTAAATATATCTACAAGAGACACTTTGATATTTGTTTTTCAC 248
                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                              OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42.8; DB 6; Length 13286;
Pred. No. 0.91;
                                                                                                                                                                                                                                                                     Length 4022;
                                                                                                                                                                                                                                                               Score 45.8; DB 6; Length 4 Pred. No. 0.11; 0; Mismatches 102; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE KEREKENCE: 4.0.75.5.
CURRENT PEDLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-0-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR APPLICATION NUMBER: DE 103100096.8
PRIOR APPLICATION NUMBER: DE 1024579.4
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2002-10-01
NUMBER OF SEQ ID NOS: 2147
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                                                                                                                                  ; NAME/KEY: unsure
; LOCATION: (1299, 1372, 1784, 3008, 3018)
; OTHER INFORMATION: unknown base
US-10-517-441-732
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Publication No. US20060121467A1
                           ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 51.2%;
Matches 107; Conservative
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RUJAN, Tamas
SCHMITT, Armin
SCHMITT, Manfred
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Best Local Similarity
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LENGTH: 13286
                                                                                                       FEATURE:
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TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel TITLE OF INVENTION: proliferative disorders FILE REFERENCE: 47675-93
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47.6%; Pred. No. 0.9;
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; Publication No. US20060121467A1
; GENERAL INFORMATION:
APPLICANT: FORKENS, John
; APPLICANT: ROENIG, Thomas
APPLICANT: MAIER, Sabine
APPLICANT: MARIER, Sabine
; APPLICANT: MARIER, Sabine
; APPLICANT: MARIER, Sabine
; APPLICANT: NIMMRICH, Inko
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SCHMITT, Armin
SCHMITT, Manfred
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MARX, Almuth
HOEFLER, Heinz
Becker, Evelyne
Lesche, Ralf
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Matches 159; Conserv
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APPLICANT: MARX, Almuth
APPLICANT: HOEFLER, Heinz
TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
TITLE OF INVENTION: proliferative disorders
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8.1%; Score 42.4; DB 6; Length 6432;
Best Local Similarity 47.6%; Pred. No. 0.9;
Matches 159; Conservative 0; Mismatches 171; Indels 4
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PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR FILING DATE: 2003-04-17
PRIOR PELING DATE: 2003-04-17
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-01
PRIOR FILING DATE: 2003-01-05
PRIOR FILING DATE: 2003-10-01
NUMBER: OF SEQ ID NOS: 2147
SEQ ID NO 606
LENGTH: 6432
                                                                                                                                                                                                                                                                             FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
CURRENT FILING DATE: 2004-12-11
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Publication No. US20060246433A1
GENERAL INFORMATION:
APPLICANT: Adorjan, Peter
APPLICANT: Burger, Matthias
APPLICANT: Maier, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                    SCHMITT, Armin
SCHMITT, Manfred
     FOEKENS, John
HARBECK, Nadia
KOENIG, Thomas
MAIER, Sabine
                                                                                                               NIMMRICH, Inko
RUJAN, Tamas
                                                                                              MODEL, Fabian
                                                                               MARTENS, John
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APPLICANT:
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1657 Aracıntınarınannancarınınınınınınanınınınınınınıngarınınınınının 1716
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                                                                                           ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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Pred. No. 1.4;
0; Mismatches 113; Indels
                                                                                                                                                                                             0; Mismatches 113; Indels
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Pred. No. 1.
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PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: EP 02004551.4
PRIOR FILING DATE: 2002-02-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 9, Application US/10506089; Publication No. US20060234224A1; GENERAL INFORMATION:
                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                  Query Match 8.0%;
Best Local Similarity 49.3%;
Matches 110; Conservative
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Best Local Similarity 49.3%;
Matches 110; Conservative
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LENGTH: 16579
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US-10-506-089-9
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TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cel
IITLE OF INVENTION: proliferative disorders
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Pred. No. 1.4;
0; Mismatches 113; Indels 0;
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                                CURRENT FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR PILING DATE: 2003-04-17
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2003-01-07
PRIOR FILING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 2147
SEQ ID NO 290
LENGTH: 16579
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FILE REFERENCE: 47675-93
CURRENT APPLICATION NUMBER: US/10/517,441
FILING DATE: 2004-12-11
PRIOR APPLICATION NUMBER: PCT/EP2003/010881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: DE 10317955.0
PRIOR PELLING DATE: 2003-04-17
PRIOR PEPLICATION NUMBER: DE 10300096.8
PRIOR PELLING DATE: 2003-01-07
PRIOR PELLING DATE: 2003-01-07
PRIOR PILING DATE: 2002-10-01
PRIOR PILING DATE: 2002-10-01
SEQ ID NO 564
CURRENT APPLICATION NUMBER: US/10/517,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 564, Application US/10517441 Publication No. US20060121467A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 49.3%;
Matches 110; Conservative (
                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
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SCHMITT, Armin
SCHMITT, Manfred
LOOK, Maxime P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: FOEKENS, John APPLICANT: HARBECK, Nadia APPLICANT: KOENIG, Thomas
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MODEL, Fabian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WAIER, Sabine
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1717 ATTTTGAAATAAGAATTAGATTTTTTAAAATAAAATTTTAAATTTTTAAATTTTTAGAT 1776
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                                                                                                                                                                                                                       ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-506-111-174
                                                                                                                                                                                                                                                                                                    Length 16579;
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                                                                                                                                                                                                                                                                                                      Query Match 8.0%; Score 42.2; DB 6; Length 1 Best Local Similarity 49.3%; Pred. No. 1.4; Matches 110; Conservative 0; Mismatches 113; Indels
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ne : 183.849 secs
PRIOR APPLICATION NUMBER: PCT/EP03/02035
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: EP02004551.4
PRIOR FILING DATE: 2002-02-27
NUMBER OF SEQ ID NOS: 1030
SEQ ID NO 174
LENGTH: 16579
                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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APPLICANT: Burger, Matthias
APPLICANT: Burger, Matthias
APPLICANT: Burger, Matthias
APPLICANT: Lesche, Ralf
APPLICANT: Cottrell, Susane
APPLICANT: Cottrell, Susane
TITLE OF INVENTION: Method and nucleic acids for the analysis of colon cell prolifera
TITLE OF INVENTION: Method and nucleic acids for the analysis of colon cell prolifera
TITLE OF INVENTION: WHERE US/10/506,089
CURRENT APPLICATION NUMBER: PGT/EP03/02034
PRIOR FILING DATE: 2003-02-27
PRIOR FILING DATE: 2003-02-27
PRIOR FILING DATE: 2002-02-27
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Publication No. US2006024643341
Publication No. US2006024643341
Publication No. US2006024643341
GENERAL INFORMATION:
APPLICANT: Adorjan, Peter
APPLICANT: Burger, Matthias
APPLICANT: Maier, Sabine
APPLICANT: Nimmrich, Inko
APPLICANT: Becker, Evelyne
APPLICANT: Lesche, Ralf
APPLICANT: Lesche, Ralf
APPLICANT: Schmitt, Armin
TITLE OF INVENTION: MISCHOOLE ACIDS FOR THE ANALYSIS OF A COLON CELL PROLIFE
TITLE OF INVENTION: DISORDER
FILE REFERENCE: 47675-84/P0994US
CURRENT APPLICATION NUMBER: US/10/506,111
CURRENT FILING DAIE: 2004-08-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 ATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCCATTTCTTTTGACGTTTTCTCTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 8.0%; Score 42.2; DB 6; Length 16579; Best Local Similarity 49.3%; Pred. No. 1.4; Matches 110; Conservative 0; Mismatches 113; Indels 0;
                                 ATTAATTGATAATTAATGAAAAATATATGTTGATAATTTT 1879
         199 ATTTGTCCTTAAATATAATCTACAAGAAGACTTTGATATTTGT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 ATTIGICCTTAAATATAATCTACAAGAAGACTTIGATATTIGI 241
                                                                                                                                                                  Sequence 19, Application US/10506089 Publication No. US20060234224A1 GENERAL INFORMATION:
APPLICANT: Adorjan, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 19
LENGTH: 16579
                                                                                                                       RESULT 14
US-10-506-089-19
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Sequence 476, App Sequence 34190, A Sequence 438, App Sequence 475, App Sequence 475

Sequence 2, Appli Sequence 474, App Sequence 474, App Sequence 475, App Sequence 2, Appli

Sequence:

Run on:

Searched:

Database

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APPLICANT: War, Samuer A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT PILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
US-09-780-669-476
US-09-822-827-476
US-09-895-814-476
US-09-895-814-476
US-10-012-895-814-476
US-10-010-940-476
US-10-10-44-678A-476
US-10-294-025-476
US-10-357-930-34190
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US-10-357-930-34190
US-10-357-930-34190
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US-10-357-930-34190
US-10-357-930-34190
US-10-205-823-438
US-09-822-827-475
US-09-895-895-793-475
US-09-895-814-475
US-010-9895-814-475
US-10-11-84-678A-475
US-10-11-84-678A-475
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US-09-957-708-2
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US-09-780-669-474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 311, Application US/09759143; Patent No. US20020022248A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (1)...(526)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Retter, Marc W.
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ORGANISM: Homo sapien
                                                                                         JS-09-759-143-311
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1: /EMC Celerra_SID83/ptodata/2/pubpna/US07_PUBCONB.seq:*
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16: /EMC_Celerra_SID83/ptodata/2/pubpna/US11B_PUBCONB.seq:*
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Sequence 21765, A
Sequence 22535, A
Sequence 27610, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 28370, A
Sequence 43052, A
Sequence 476, App
                                                                                                                                                  December 31, 2006, 12:22:01; Search time 837.563 Seconds (without alignments) 7716.790 Million cell updates/sec
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Sequence 311, R
Sequence 311, R
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Sequence 311, 1
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Sequence 311, 1
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Sequence 311,
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                                                                                                                                                                                                                                         US-09-232-880-311
525
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                          GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-357-930-22535
US-10-357-930-27610
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US-09-780-669-311
US-09-232-887-311
US-09-232-880-311
US-09-895-793-311
US-10-012-896-311
US-10-010-940-311
US-10-144-678A-311
US-10-294-025-311
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Gapop 10.0 , Gapext 1.0
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: Hural, John
APPLICANT: Hushin, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton: CoMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
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                           Indels
            Pred. No. 6.7e-113;
; Mismatches 0;
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Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                            526; Conservative
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            Best Local Similarity
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; Sequence 311, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
    APPLICANT: W. Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFREENCE: 2011.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FASISEQ for Windows Version 3.0
; SEQ ID NO 311
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Best Local Similarity 100.0%; Score 525; DB 3; Length 526;
Best Local Similarity 100.0%; Pred. No. 6.7e-113;
Matches 526; Conservative 0; Mismatches 0; Indels
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NAME/KEY: misc feature
LOCATION: (1)...(526)
CTHER INFORMATION: n = A,T,C or G
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TYPE: DNA
ORGANISM: Homo sapien
FRATURE:
MAME/KEY: misc_feature
LOCATION: (1)...(526)
OTHER INFORMATION: n = A,T,C or
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ORGANISM: Homo sapien
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APPLICANT: MCNeil, Patricia D.
APPLICANT: HURLAL, Obn
APPLICANT: HURLAL, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE REFERENCE: 210121.534C2
CURRENT PAPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 311
LENGTH: 526
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Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Jiang, Yuqiu
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Dav. Craig H.
APPLICANT: Carter, Dav. Craig H.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
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Hepler, William T.
Henderson, Robert A.
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ORGANISM: Homo sapien
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                                                Gaps
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US-09-232-880-311

Sequence 311, Application US/09232880

Publication No. US20020182596A1

GENERAL INFORMATION:

APPLICANT: Millon, Davin C.

APPLICANT: Millon, Dannifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF

TITLE REFRENCE: 210121.428C6

CURRENT RILING DATE: 1999-01-15

NUMBER OF SEQ ID NOS: 338

SEQ ID NO 311

LENGTH: 526
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100.0%; Score 525; DB 3; Length 526; 100.0%; Pred. No. 6.7e-113;
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100.0%; Score 525; DB 3; L
Best Local Similarity 100.0%; Pred. No. 6.7e-113;
Matches 526; Conservative 0; Mismatches 0;
                                             0; Mismatches
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OTHER INFORMATION: n = A,T,C or
                      Best Local Similarity 100.0%;
Matches 526; Conservative (
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY ITILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FASISEQ for Windows Version 3.0
SEQ ID NO 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 AGTICTATAAACTGTAGTNTACTTATTTTAATCCCCAAAGCACAGT 526
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100.0%; Pred. No. 6.7e-113;
trive 0; Mismatches 0;
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APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (1)...(526)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 526; Conservative
                                                                                                                                               LENGTH: 526
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                ; OTHER INFORMAT
US-09-895-814-311
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US-10-012-896-311
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100.0%; Pred. No. 6.7e-113;
iive 0; Mismatches 0;
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020193296A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Miccham, Jennifer L.
APPLICANT: Micham, Jennifer L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Red'ick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Li, Samuel X.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
       ; NAME/KEY: misc_feature
; LOCATION: (1)...(526)
; OTHER INFORMATION: n = A,T,C or
US-09-895-793-311
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Fanger, Gary R.
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NAME/KEY: misc_feature
LOCATION: (1)...(526)
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APPLICANT: Mantenabe, Yoshihiro
APPLICANT: Mantenabe, Yoshihiro
APPLICANT: Madaber, Madabeine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 21011.437C27
CURRENT APPLICATION NUMBER: US/10/012,896
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTICIATAAACIGIAGINTACITAITITAAICCCCAAAGCACAGT 526
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                                                                                                                                     Houghton, Raymond L.
Vinals de Bassols, Carlota
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                                             Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
                                                                                                              McNeill, Patricia D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%;
Matches 526; Conservative 0
Carter, Darrick
                , Samuel X.
                                Wang, Aijun
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                      Foy, Teresa
                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 311
LENGTH: 526
                                                             APPLICANT:
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181 ATTAAACATGGAATAAAGATTTGTCCTTAAATATAATCTACAAGAAGACTTTGATATTTG 240
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                                                                                                                                                 APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Redes, Michael
APPLICANT: Reter, Mark
APPLICANT: Retter, Mark
APPLICANT: Retter, Mark
APPLICANT: Banger, Gary
APPLICANT: Oby, Craib
APPLICANT: Day, Craib
APPLICANT
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100.0%; Score 525; DB 6; L
Best Local Similarity 100.0%; Pred. No. 6.7e-113;
Matches 526; Conservative 0; Mismatches 0;
Sequence 311, Application US/10010940 Publication No. US20030088062A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: n = A,T,C or G
US-10-010-940-311
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TITITICACAAGIGAAGCATICITAIAAAGIGICATAAACCTITITIGGGGAAACIAIGGGAA 300
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                                                                                               ACAGCAAGAGCTTCTCATCTAAACCCTTTTCCCTTTTTAGTATCTGTGTATCAAGTATAAA 480
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Sequence 311, Application US/10294025
Sequence 311, Application US/10294025
Publication No. US20030185830A1
GENERAL INFORMATION:
APPLICANT: Xt, Jiangchun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER;
FILE REFERENCE: 210121.427C29
CURRENT APPLICATION NUMBER: US/10/294,025
CURRENT APPLICATION NUMBER: US/10/294,025
SOFTWARE: FastSEQ for Windows Version 3.0
SSQ IN NO 311 S26

LENGTH: 526
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Best Local Similarity 100.0%; Pred. No. 6.7e-113;
Matches 526; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 499
COTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Notals y de Bassols, Carlota
APPLICANT: Notals y de Bassols, Carlota
APPLICANT: Watenabe, Yoshihiro
APPLICANT: Watenabe, Yoshihiro
APPLICANT: Deng, Ta
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 21012.1427C28
CURRENT APPLICATION NUMBER: US/10/144,678A
CURRENT APPLICATION NUMBER: US/10/144,678A
SOFTWARE: FASESO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 525; DB 7; Length 526; Best Local Similarity 100.0%; Pred. No. 6.7e-113; Matches 526; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Hural, John
McNeill, Parricia D.
Houghton, Raymond L.
Vinals y de Bassols, Carlota
Foy, Teresa M.
Watanabe, Yoshihiro
          Sequence 311, Application US/10144678A Publication No. US20030157089A1 GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun APPLICANT: Mitcham, Jennifer L. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Henderson, Robert A. APPLICANT: Henderson, Robert A. APPLICANT: Fanger, Wichael D. APPLICANT: Fanger, Michael D. APPLICANT: Fanger, Michael D. APPLICANT: Fanger, Cary R. APPLICANT: Stolk, John A. APPLICANT: Carter, Darrick APPLICANT: Garter, Darrick APPLICANT: Mang, Aljun APPLICANT: Skeiky, Yasair A. W. APPLICANT: Hepler, William T. APPLICANT: Hopler, William T. APPLICANT: Hopler, William T. APPLICANT: Hopler, William T. APPLICANT: Hopler, William T. APPLICANT: Houghton, Raymond L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 499 OTHER INFORMATION: n = A, T, C or G
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LENGTH: 526
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                                                                                                                                                                                            121 CATITACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
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                                                             CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA
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; LOCATION: 1, 7, 9, 11, 1199; 1200, 1201, 1202, 1203

; CTHER INCRMATION: n = A,T,C or G

US-10-357-930-21765
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APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: IDENTIFICATION, ASSESSMEN
TITLE OF INVENTION: IDENTIFICATION, ASSESSMEN
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-OOTBCN
CURRENT FILING DATE: 2003-02-04
PRIOR PELLOATION NUMBER: 09/785,276
PRIOR PELLOATION NUMBER: 09/785,276
PRIOR PELLOATION NUMBER: 60/183,319
PRIOR PELLOATION NUMBER: 60/183,319
PRIOR PILING DATE: 2000-03-16
PRIOR PELLOATION NUMBER: 60/183,462
PRIOR PELLOATION NUMBER: 60/183,462
PRIOR PELLOATION NUMBER: 60/213,314
PRIOR PELLOATION NUMBER: 60/211,314
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR PELLING DATE: 2000-06-09
PRIOR PELLING DATE: 2000-06-09
PRIOR PELLING DATE: 2000-07-18
PRIOR PELLING DATE: 2000-07-18
PRIOR PELLING DATE: 2000-07-18
PRIOR PELLING DATE: 2000-07-18
PRIOR PELLING DATE: 2000-12-13
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21765
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; Publication No. US20040259086A1
; GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
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421 ACAGCAAGAGCTTCTCATCTAAACCCTTTCCCTTTTTAGTATCTGTGTATCAAGTATAAA 480
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APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasin A.
TITLE OF INVENTION: POLYEPTIDES THEREOF
FILE REFERENCE: 210121.427031
CURRENT APPLICATION WUMBER: US 09/568.857
PRIOR PELLING DATE: 2005-09-23
PRIOR PELLING DATE: 2000-05-09
PRIOR PELLING DATE: 2000-01-14
PRIOR PELLING DATE: 2000-01-14
PRIOR PELLING DATE: 1999-01-12
PRIOR PELLING DATE: 1999-01-13
PRIOR PELLING DATE: 1999-01-13
PRIOR PELLING DATE: 1999-01-15
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                                                        AGTICIATAAACIGIAGINTACTIATITIAAICCCCAAAGCACAGT 526
                                                                                                             481 AGTICTATAAACTGTAGTNIACTIATTTTAATCCCCAAAGCACAGT 526
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100.0%; Pred. No. 6.7e-113;
tive 0; Mismatches 0;
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NUMBER OF SEQ ID NOS: 701
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                    Sequence 311, Application US/11234786 Publication No. US20060024301A1 GENERAL INFORMATION:
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OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                       APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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Reed, Steven G.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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PRIOR FILING DATE: 1998-02-25
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Best Local Similarity 100.
Matches 526; Conservative
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ORGANISM: Homo sapien
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LENGTH: 526
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APPLICANT:
APPLICANT:
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RESULT 14
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Sequence 22555. Application US/10357930

Publication No. USC0040259086A1

GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Bndege, Wilson
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: UDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: UDENTIFICATION NUMBER: US/10/357,930
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
FRIOR FILING DATE: 2000-02-16
FRIOR FILING DATE: 2000-03-16
FRIOR APPLICATION NUMBER: 60/189,862
FRIOR APPLICATION NUMBER: 60/189,862
FRIOR APPLICATION NUMBER: 60/211,314
FRIOR FILING DATE: 2000-03-16
FRIOR APPLICATION NUMBER: 60/211,314
FRIOR APPLICATION NUMBER: 60/211,314
FRIOR FILING DATE: 2000-05-25
FRIOR FILING DATE: 2000-05-05
FRIOR FILING DATE: 2000-05-18
FRIOR FILING DATE: 2000-05-18
FRIOR FILING DATE: 2000-05-18
FRIOR FILING DATE: 2000-07-18
FRIOR FILING DATE: 2000-07-18
FRIOR FILING DATE: 2000-07-18
FRIOR FILING DATE: 2000-12-13
FRIOR FILING DATE: 2000-13-13
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                                                                                                                            342 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC 401
                                                                                                                                                                                      120
                                                                                                                                                                                                              TITIGACGITITICICIAAACTACTAAAGAGGCATIAAIGAICCAIAAAITAITAITAITAA 461
                                                                                                                                                                                                                                                                      CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
                                                                                                                                                                                                                                                                                                                                                                                            581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              701
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                                                                                                                                                                                                                                                                                                                                                                             582 TITITCACAAGTGAAGCATTCTTATAAAGTGTCATAACCTTTTTGGGGAAACTATGGGAA
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                                                                                                       CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCCATTTC
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                                                              3;
                   Length 1203;
                                                              Indels
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                   90.9%; Score 477.2; DB 9; 98.8%; Pred. No. 1.6e-101; ive 0; Mismatches 3;
            Query Match
Best Local Similarity 98.8
Marches 512; Conservative
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Sequence 27610, Application US/10357930

Sequence 27610, Application US/10357930

Publication No. US20040259086A1

GENERAL INFORMATION:

APPLICANT: Schlegel. Robert

APPLICANT: Endege, Wilson

APPLICANT: Endege, Wilson

APPLICANT: MONDHAR, JOHN BROSTATE

TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMAN PROSTATE CANCER

TITLE OF INVENTION: HUMBER: US/10/357,930

CURRENT APPLICATION NUMBER: US/10/357,930

CURRENT FILING DATE: 2003-02-04

PRIOR FILING DATE: 2000-02-17

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR APPLICATION NUMBER: 60/183,319

PRIOR APPLICATION NUMBER: 60/207,454

PRIOR PILING DATE: 2000-03-16

PRIOR PILING DATE: 2000-05-25

PRIOR APPLICATION NUMBER: 60/207,454

PRIOR APPLICATION NUMBER: 60/207,454
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1, 7, 9, 11, 1199, 1200, 1201, 1202,
OTHER INFORMATION: n = A,T,C or G
US-10-275-330-22535
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ORGANISM: Homo sapiens
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Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TILLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF TILLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
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NAME/KEY: misc_feature

LOCATION: 1, 7, 9, 11, 1199, 1200, 1201, 1202, 1203

CTHEN THORNATION: n = A,T,C or G

US-10-357-930-27610
                                                                                                                                                                                                                                                                                                Score 477.2; DB 9;
Pred. No. 1.6e-101;
0; Mismatches 3;
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/219,007
; PRIOR FILING DATE: 2000-07-18
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 62232
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27610
; LENGTH: 1203
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Best Local Similarity 98.8%;
Matches 512; Conservative
                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: 1, 7, 9, 11, 1199, 1200, 1201, 1202, 1203

; CIHER INFORMATION: n = A,T,C or G

US-10-357-930-28370
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Pred. No. 1.6e-101;
0; Mismatches 3;
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR PILING DATE: 2000-02-17
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-05-25
PRIOR PILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-12-13
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Best Local Similarity 98.8
Matches 512; Conservative
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AL17569¢ Tetraodon
AL070972 Drosophil
AG201107 Pan trogl
AG368405 Mus muscu
AL106896 Drosophil
AL106896 Drosophil
BE56331 pacs2-164
AL069706 Drosophil
CC264939 CH261-19L
AL069706 Drosophil
AL069707 Drosophil
AL069707 URSG1-19L
AG526131 Mus muscu
AL063921 Drosophil
AL071298 Drosophil
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Query Match

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ORIGIN

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478 bp DNA linear GSS 09-JUN-1998 CIT-HSP-2301D2,TF CIT-HSP Homo sapiens genomic clone 2301D2, AQUI5128
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1 (bases 1 to 478)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGAGAAGCTAAATAA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTTCACAAGTGAAGCATTCTTATAAAGTGTCATAACCTTTTTGGGGAAACTATGGGAA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                                                                                                                                                                  220 TTTTTCACAAGTGAAGCATTCTTATAAAGTGTCATAACCTTTTGGGGGAAACTCTGGG-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGAAGCTAAATAA
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                                                                                                                                                                                                                                                                                                                                                                     1 CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC
                                                                                                                                                                                                Length 678;
                                                                        /clone="PTB-094J13.F"
/sex="male"
/cell_type="lymphoblast"
/clone_llb="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                           20; Indels
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                                                                                                                                                                                                Score 335; DB 14;
Pred. No. 9.8e-68;
0; Mismatches 20;
            /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, 17e1: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Building (1998)
Unpublished (1998)
Other_GSS8: CIT-HSP-2301D2.TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTCTTTACAGGGAGCTCC 379
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                                                                                                                                                                                                   Query Match 63.8%;
Best Local Similarity 94.5%;
Matches 358; Conservative 0
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Homo sapiens
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Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (O2-MGG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbesegac.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170,

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       678 bp DNA linear GSS 03-NOV-200
Pan troglodytes DNA, clone: PTB-094J13.F, genomic survey sequence.
AG093969
AG093969.1 GI:16645771
GSS.
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Pan troglodytes
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                  CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGAAGCTAAAATAA
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                                                                                                                        Gaps
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                        ;
0
                                                                             68.8%; Score 361.4; DB 14; Length 684; llarity 97.1%; Pred. No. 6.4e-74; Conservative 0; Mismatches 11; Indels 0;
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                                Best Local Similarity
Matches 368; Conserv
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KEYWORDS SOURCE ORGANISM

TITLE JOURNAL REFERENCE

AUTHORS

AUTHORS

REFERENCE

TITLE

COMMENT

FEATURES

RESULT 2 AG093969/c DEFINITION ACCESSION VERSION

180

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401

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Gaps

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/sex="Female
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Matches 238; Conserv
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I (bases 1 to 597)

S Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
Radelof,U. Schneider,D. and Korn,B.
Human UnigeneSet - RZPD3

L Unpublished (2003)

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
IM Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAG999810228.

RZPDIB; I.M.A.G.E. cDNA Clone Collection;
Human UnigeneSet - RZPD3 (RZPDLIB No.972)
http://www.rzpd.de/CloneCards/Ggi-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 CATITACAGCATITAAAATGTGTTCAGCATGAAATATTAGCTACAGGGTAAGCTAAATAA 231
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                               CAAATTTGAGCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTC
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                       1. .478

/ Organism="Homo sapiens"

/ nol type="genomic DNA"

/db_xref="taxon:606"

/ clone="231D2"

/ sex="Male"

/ cell type="Sperm"

/ clone lib="CIT-HSP"

/ note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII
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BX098119 Scares placenta Nb2HP Homo sapiens cDNA clone
IMAGP998102228 ; IMAGE:149065, mRNA sequence.
                                                                                                                                                                                                                                                                                                  Score 289; DB 11; Length 478; Pred. No. 5.6e-57; 0; Mismatches 20; Indels
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                                                        Location/Qualifiers
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93.6%;
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Homo sapiens
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Best Local Similarity
Matches 323; Conserv
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AA843706 524 bp mRNA linear EST 31-DEC-1998 aj42£05.81 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1392993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 CAAATTTGAGCCAATGACATAGAATTTACAAATCAAGAAGCTTATTCTGGGGC--ATTT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 CTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATATTATATATTATTATTATCTA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAATAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ATTAAACATGGAATAAAGATTTGTCCTTAAATATATAATCTACAAGAAGACTTTGATATTTG 240
Tel: +49 30 32639 101
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTTGACGTTTTCTCTAAACTACTAAAGAGGCATTAATGATCCATAAATTATATTATCTA
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Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42.7%; Score 224.2; DB 4; Length 597; ilarity 97.9%; Pred. No. 8.6e-42; Conservative 0; Mismatches 3; Indels 2;
                                                                                                                                                                                                                                                                                                clone="IMAGp998I02228 ; IMAGE:149065"
                                                                                                                                                                                                                     organism="Homo sapiens"
                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCT-CGAP clone distribution information can be
cloud through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/limage.html
Insert Length: 948 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 474.

1. 524
                                                                                                                                                                                                                                                                                /lab_host="DH10B"
/clone lib="Soares testis NHT"
/clone lib="Soares T773D-PacI; Site_1: Not I; Site_2: Eco RI;
/note="Vector: pT773D-PacI; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was prepared from mRNA obtained from
Clontech Laboratories, Inc., and primed with a Not I -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 14-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 CATITACAGCATITAAAAIGIGITICAGCAIGAAATAITAGCIACAGGGGAAGCIAAAIAA 483
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Lobases 1 to 360)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultenn,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 bp mRNA linear EST yj18b01.rl Soares placenta Nb2HP Homo sapiens CDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 216.2; DB 1,
Pred. No. 6.3e-40;
0; Mismatches 3;
                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAGE:149065 5', mRNA sequence.
                                                                                                                                                                                                                                                  clone="IMAGE:1392993"
                                                                                                                                                                                                             'mol_type="mRNA"
'db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                            oligo(dT) primer [5
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Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.6%;
Matches 218; Conservative
                                                                                                                                                                                                                                                                       sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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Sonaldo, Ph.D.
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ORGANISM
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COMMENT
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In (Dasses 1 to 301)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silvay, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Ragal, M.A., G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST 11-SEP-2000 mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 AATTTGAGCCCAATGACATAGAATTTTACAAATCAAGAAGCTTATTCTGGGGC--ATTTC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                                                                                                                                                                    Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL , contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 694 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 TITGACGITITCICTAAACTACTAAAGAGGCATTAATGATCCATAAATTATATCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145 TITGACGITITCICIAAACIACIAAAAGAGGCATIAATGAICCAIAAAITAIAITATCIAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AAATTTGAGCCAATGGAGAATTTTACAAATCAAGAAGCTTATTCTGGGGCCATTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 ATTTACAGCATTTAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAAGCTAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 694
High quality sequence stops: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 bp mRNA linear
PMO-BT0757-240500-003-D01 BT0757 Homo sapiens cDNA,
BE694624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.9%; Score 178.2; DB 10; Length
95.1%; Pred. No. 4.8e-31;
ive 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
                                                                                                                                                                                                                                          Insert Length: 694 Std Error:
Seq primer: MISRPI
High quality sequence stop: 238.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTAAACATGGAATAAAGATTTGTCC 206
                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="GDB:560899"
                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:149065"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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Matches 195, Conservative
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JOURNAL PUBMED

COMMENT

TITLE

FEATURES

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/dev stage="45 years old"
//dev stage="45 years old"
//dev stage="15 years old"
//debost="DHLOB"
//dlon=lib="NCI_CGAP_Pr3"
                                                                                               Email: cgapbs-remail.nin.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 890 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stops: 325.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 ATACAGAAATGAGTGGCTGGAGATTCTTGATTGCATAGC-AGAGCTTCTCATCTAAAACCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 AGTATCTTACCTGAAGCTACAGACTCCATAACCTCTTTTACAGGGAGCTCCTGCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 AGTGGGTTCCCTGAAGCTACAGACTCCATAACCTCTTTAGAGGGAGCTCCTGCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        448 ITCCCTTTTTAGTATCTGTATCAAGTATAAAAGTTCTATAAAACTGTAGTNTACTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 TTCCCTTTTTAGTGTCTGTGTATC-AGTATAAAAGTTCTATAAAACTGTAGTTACTGTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 145.2; DB 1;
Pred. No. 2.6e-23;
0; Mismatches 14;
                                                                         Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .462
/organism="Homo sapiens
/mol_type="mRMA"
/db_xref="taxon:9606"
/clone="IMAGE:953485"
                                                                     Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 27.7%; al Similarity 91.6%; 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.
1 (bases 1 to 288)
                                Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   508 TTAATCCCCAA 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTAATCCCAAA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 175; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE827798
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ORGANISM
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                                        JOURNAL
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BE827798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM0-BT0757-240
SGQ primer: puc 18 forward
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=__organ: breast; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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nh26d07.s1 NCI_CGAP_Pr3 Homo sapiens CDNA clone IMAGE:953485, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 AACCTCTCTTTACAGGGAGCTCCTGCAGCCCCTACAGAAATGAGTGGCTGAGATTCTTGA 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGCACAGCAAGAGCTICTCAICTAAACCCTITICCCTITITAGTAICTGTGTAICAAGTA 476
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Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae, Homo.
1 (bases 1 to 462)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 GGAAAAATGGGGAAACTCTGAAGGGTTTTAAGTATCTTACCTGAAGCTACAGACTCCAT
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                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
10737800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477 TAAAAGTTCTATAAACTGTAGTNTACTTATTTTAATCCCCAA 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.8%; Score 166.8; DB 7
93.2%; Pred. No. 2.2e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .301
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BT0757"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stringency conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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AA528286.1 GI:2270355
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Matches 207; Conservative
                                                                                                          sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
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Query Match

ORIGIN

417 125

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183

RESULT 8 AA528286/c DEFINITION VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS TITLE

387 375 447 316 507 257

Gaps

5.

COMMENT

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/lone lib="NOI CGAP Pr28"
/clone lib="NOI CGAP Pr28"
/note="Organ: prostate; Vector: pT7T3D-PacI; Plasmid DNA from the normalized library NCI CGAP Pr22 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and li217928-1220615). Subtraction by Bento Soares and M. Patima Bonaldo. "
                                                                                                                                                                                                             Email: cgapbe-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing Dy: Washington University Genome Sequencing Center
DNA Sequencing Dy: Washington University Genome Sequencing Center
Clone distribution: NI-CGAP Cone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 432.
High quality sequence stop: 432.
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nh32h04.s1 NCI_CGAP_Pr3 Homo sapiens CDNA clone IMAGE:954103, mRNA
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Mammalia, Eutheria, Buarchontoglires, Primates, Catarrhini;
                                                                                                                   (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTACCTGAAGCTACAGACTCCATAACCTCTTTACAGGGAGCTCCTGCAGCCCCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 AAATGAGTGGCTGAGATTCTTGATTGCACAGGAGCTTCTCATCTAAACCCTTTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                    Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini;
                                        Hominidae, Homo.
1 (bases 1 to 554)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7; Length 554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 144.2; DB 7;
Pred. No. 4.6e-23;
0; Mismatches 3;
                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3310770"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
/lab_host="DH10B"
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96.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
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                                                                                                                                               Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
ses 179; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             514 CCCAA 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAAA 506
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AA525072/c
LOCUS
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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7959c10.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3310770 3', BF001177
                                                                                                                                                                                                                                                                                                                                                                                                               Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC2-ET0022-170
500-015-all&t3=2000-05-17&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence stop: 288.
Location/Qualifiers
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 TTTTAGTGTCTGTGTATC-AGTATAAAAGTTCTATAAAACTGTAGT-TACTTATTTTAATC 264
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                         Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 TTACCTGAAGCTACAGACTCCATAACCTCTTTACAGGGAGCTCCTGCAGCCCCTACAG
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                       Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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KEYWORDS
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NISC gj11g01.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:3271488 CB049577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   493 TGAGTGGCTGAGATTCTTGATAGCATAGC-AGAGCTTCTCATCCAAACCCTTTCCCTTNT 435
                                                                                                                                                                                                 High Throughput Sequenting Center University of Mashington University of Mashington 401 Queen Anne Avenue North, Seattle, WA 98109, USA 1911: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 616-3887
Email: juallaceedu.washington.edu
Ender may be purchased from Research Genetics (info@resgen.com)
EAC end Web Server: http://www.htsc.washington.edu
Seq primer: T7
Class: BAC ende
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 577)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
/clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                    Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 10449764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397 TGAGTGGCTGAGATTCTTGATTGCACAGGAGGCTTCTCATCTAAAACCCTTTCCCTTTT
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
cDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="plate=3167 Col=22 Row=H"
                                                                                                                                                                              Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23.6%; Score 124; DB 11;
91.1%; Pred. No. 2.5e-18;
iive 0; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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Location/Qualifiers
1. .559
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Homo sapiens
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Matches 163; Conservative
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CB049577
       AUTHORS
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//clone lib="NCI_CGAP Pr3"
//otoe="Vector: pAMP10; Site_1: Not1; Site_2: EcoR1; 1st
strand cDNA was primed with Oilgo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from
5,000-10,000 microdissected cells
histologically-determined to be fully malignant prostate
cancer cells. Double-stranded cDNA was ligated to EcoR1
adaptors, 5 cycles of PCR applied to the cDNA with an
adaptors specific primer, and the resulting PCR product
subcloned into pAMP10 by the UDG-cloning method (Life
Technologies). Average insert size is 600 bp. NOTE: Not
directionally cloned. This library was constructed by
                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissaue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
Tissaue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
Tissaue Procurement: W. Marston Linehan, Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40ml3 fwd. ET from Amersham.

Location/Qualifiers
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HS_3167_B2_D11_T7C_CIT_Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3167_Col=22 Row=H, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTACCTGAAGCTACAGACTCCATAACCTCTTTACAGGGAGGTCCTGCAGGCCCCTACAG 393
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
                       1 (bases 1 to 265)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="45 years old"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:954103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTTAGTATCTGTGTATCAAGT 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   David Krizman.
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AQ802217
AQ802217.1 GI:5719549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
Homo sapiens
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1 (bases 1 to 559)
                                                                                                       Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . . 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334
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AQ802217/c
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: Saci
: Saci
Email: ekirknes@tigr.org
Class: shotgun.
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                                                                                                                                                                                                                                               Best Local Similarity 73.1
Matches 185; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 TAATATTTGTTT 1
                                                    1. 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes
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R.Site 1
R.Site 2
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AG056621
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                                                                                                                                                                                                                                           /clone_lb="NCIC CGAP_Pr28"
/note="Organ: prostate; Vector: pT773D-PacI; Plasmid DNA from the normalized library NCI CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hypridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDS 985608-986759, 1101192-1101959, and Farina Ronaldo. "Batina Ronaldo."
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov. Plate: LLAM8008 row: N column: 1 Seq primer: -21M13 forward primer (ABI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Kirkness BF
The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 bp DNA linear GSS 27-SEP-200 tigr-gss-dog-17000334478329 Dog Library Canis familiaris genomic, genomic, genomic, genomic, grans, survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 AAATGAGTGGCTGAGATTCTTGATTGCACAGCAAGAGCTTCTCATCTAAACCCTTTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATGAGTGGCTGAAATTTTTGATTGCACAACAA-AACTTTTTCATCTAAACCCTTTCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The dog genome: survey sequencing and comparative analysis Science 301 (5641), 1898-1903 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 577;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.3%; Score 122.4; DB 4
89.7%; Pred. No. 5.9e-18;
iive 0; Mismatches 16,
                                                                                                       1. :577
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3271488"
                                                                                                                                                                                                            /dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CE393091
CE393091.1 GI:36634243
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Canis familiaris
                                                                                                                                                                                               sex="male"
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1 (bases 1 to 434)
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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Direct Submission

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbesegercriken.go.jp, Wit:http://hgp.gsc.riken.go.jp/,
Tel:91-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the RkD process and may have higher chance of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 CTTTTTAAGTTCTTTCTAAGCTACTCAAGAGGCAACTGGTTCTCCATAAATTATATCATC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTAAATAAATTAAACATGGAATAAAGATTTGTCCTTAAATATAATATCTACAAGAAGACTT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGUSE621 709 bp DNA linear GSS 02-NOV-200:
Pan troglodytes DNA, clone: PTB-042P10.F, genomic survey sequence.
AG056621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 TACATTTACAGCATT-----TAAAATGTGTTCAGCATGAAATATTAGCTACAGGGGAA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 CAAACTTGAGTTAATGGCACAGAATTTTACAAGATCAAAAAGCTTCATCTAGAGCATTT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTAAGTAAATTAACAGGGAATAAAGGCTTTGATCTTAAAAAATCATTACCAGAAAGATCT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 TACCITTACAGGATTAAAAAAAAAATGTGTTGGGCATGCAACATTAGCCTCAGTGTTA 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTTTGACGTTTTCTCTAAAGTACTAAAGAGGC-ATTAATGATCCATAAATTATATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAAATTTGAGCCAATGACATAGAATTTTACAA-ATCAAGAAGCTTATTCTGGGGCCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                        Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                         21.1%; Score 110.6; DB 12; Length 434; 73.1%; Pred. No. 3.3e-15; Live 0; Mismatches 59; Indels 9;
                                                                                     /organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
shotgun.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglodytes (chimpanzee)
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LIBRARY
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340 GAAGCTACAGACTCCATAACCTCTTTACAGGGAGCTCCTGCAGCCCCTACAGAAATGA 399
                                                                                                                                                                                                                                                                                3; Gaps
Location/Qualifiers

1. 709
| crganise="Pan troglodytes"
| do_type="genomic DNA"
| db_xref="taxon:9598"
| clone="prB-042Pl0.F"
| sex="male" lymphoblast"
| clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                   Query Match
Best Local Similarity 78.8%; Pred. No. 1.2e-09;
Matches 141; Conservative 0; Mismatches 35; Indels
                source
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